

Annex 1

**PBP2X AMINO ACID SEQUENCE ACCESSION NUMBERS
AVAILABLE IN THE SEQUENCE DATA BASES
AT THE PRIORITY DATE (11 JULY 2002)**

1PMD
P14677
AAC45547
AAC95456
AAD45394
AAF17263
AAF17264
AAF17265
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CAA67013
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CAC43045

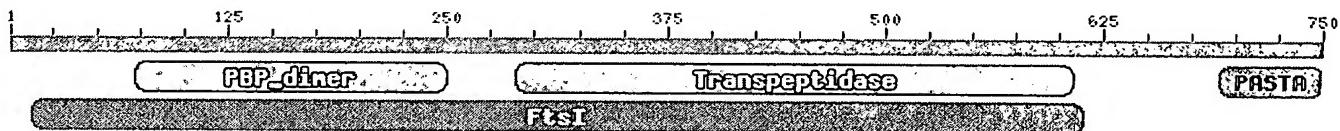
BLAST Basic Local Alignment Search Tool

Job Title: PBP2X-R6

Annex 2

Show Conserved Domains

Putative conserved domains have been detected, click on the image below for detailed results.



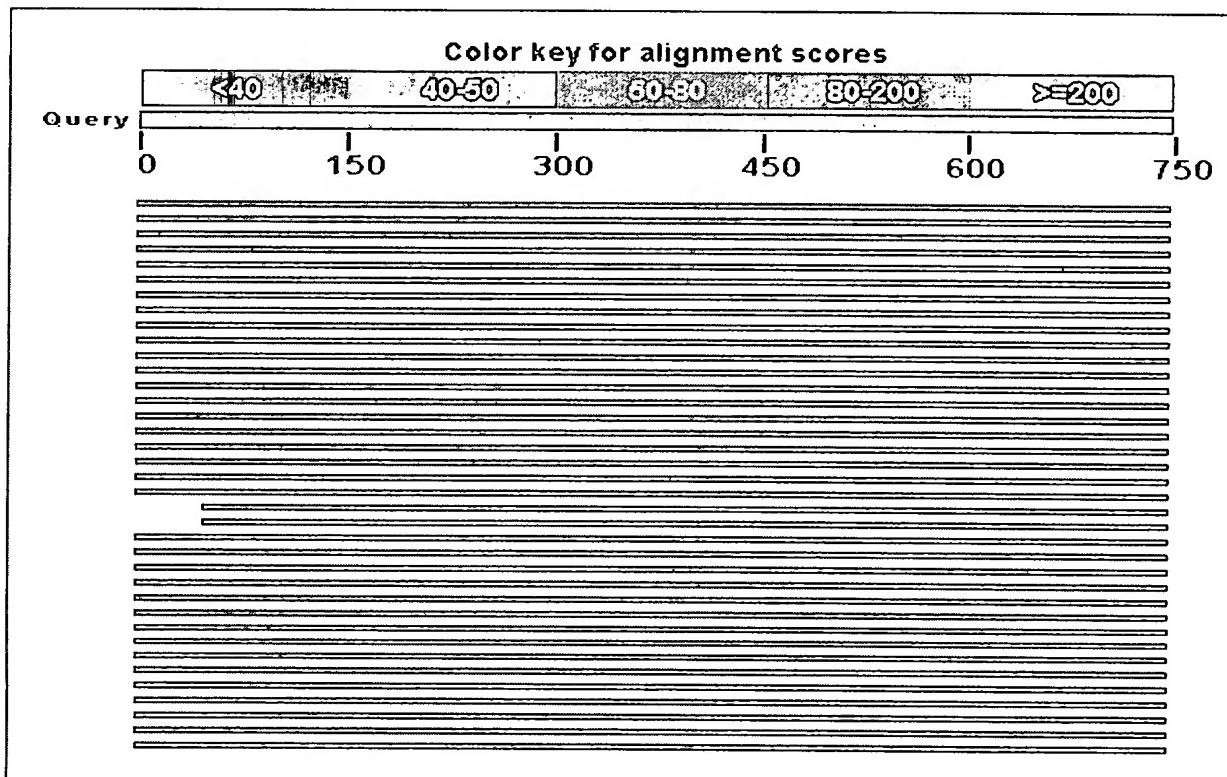
-
- Your search is limited to records matching entrez query: PBP2x penicillin binding protein AND Streptococcus pneumoniae [ORGN].
-

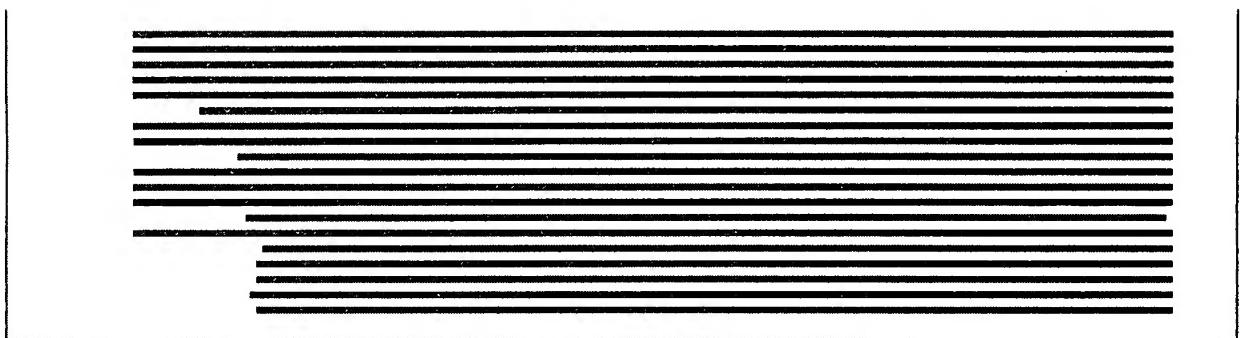
BLASTP 2.2.16 (Mar-25-2007)

Reference: Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schäffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997), "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs", Nucleic Acids Res. 25:3389-3402.

Reference: Schäffer, Alejandro A., L. Aravind, Thomas L. Madden, Sergei Shavirin, John L. Spouge, Yuri I. Wolf, Eugene V. Koonin, and Stephen F. Altschul (2001), "Improving the accuracy of PSI-BLAST protein database searches with composition-based statistics and other refinements", Nucleic Acids Res. 29:2994-3005. RID: 5ZZGCTZA015 Database: All non-redundant GenBank CDS translations+PDB+SwissProt+PIR+PRF excluding environmental samples from WGS projects 4,990,428 sequences; 1,725,524,515 total letters

Query= Length=750

Distribution of 100 Blast Hits on the Query Sequence



Distance tree of results [NEW](#) Related Structures

Sequences producing significant alignments:		Score (Bits)	E Value
sp P59676 PBPX_STRR6 Penicillin-binding protein 2X (PBP-2X) (PBP	1441	0.0	G
dbj BAD00902.1 penicillin-binding protein 2X [Streptococcus pne	1439	0.0	
dbj BAD67448.1 penicillin-binding protein 2X [Streptococcus pne	1438	0.0	
sp P14677 PBPX_STRPN Penicillin-binding protein 2x (PBP-2x) (PBP	1438	0.0	
dbj BAD00901.1 penicillin-binding protein 2X [Streptococcus pne	1438	0.0	
dbj BAD00904.1 penicillin-binding protein 2X [Streptococcus pne	1436	0.0	
gb AAF17263.1 AF210753_1 penicillin-binding protein 2X [Streptoc	1434	0.0	
dbj BAD00905.1 penicillin-binding protein 2X [Streptococcus ...	1418	0.0	
dbj BAD00912.1 penicillin-binding protein 2X [Streptococcus pne	1415	0.0	
gb AAF17266.1 AF210756_1 penicillin-binding protein 2X [Streptoc	1397	0.0	
gb AAF17265.1 AF210755_1 penicillin-binding protein 2X [Strep...	1395	0.0	
dbj BAD00920.1 penicillin-binding protein 2X [Streptococcus pne	1368	0.0	
dbj BAD00903.1 penicillin-binding protein 2X [Streptococcus pne	1367	0.0	
dbj BAD00916.1 penicillin-binding protein 2X [Streptococcus pne	1365	0.0	
gb AAF17267.1 AF210757_1 penicillin-binding protein 2X [Streptoc	1361	0.0	
dbj BAD00919.1 penicillin-binding protein 2X [Streptococcus pne	1357	0.0	
gb AAF17264.1 AF210754_1 penicillin-binding protein 2X [Streptoc	1349	0.0	
dbj BAD00929.1 penicillin-binding protein 2X [Streptococcus pne	1348	0.0	
dbj BAD00909.1 penicillin-binding protein 2X [Streptococcus pne	1345	0.0	
dbj BAD00907.1 penicillin-binding protein 2X [Streptococcus pne	1344	0.0	
pdb 1QME A Chain A, Penicillin-Binding Protein 2x (Pbp-2x) >p...	1344	0.0	S
pdb 1PYY A Chain A, Double Mutant Pbp2x T338aM339F FROM STREP...	1341	0.0	S
dbj BAD00918.1 penicillin-binding protein 2X [Streptococcus pne	1340	0.0	
dbj BAD00910.1 penicillin-binding protein 2X [Streptococcus pne	1336	0.0	
dbj BAD00923.1 penicillin-binding protein 2X [Streptococcus ...	1327	0.0	
dbj BAD00917.1 penicillin-binding protein 2X [Streptococcus pne	1324	0.0	
dbj BAD00927.1 penicillin-binding protein 2X [Streptococcus pne	1323	0.0	
dbj BAD00913.1 penicillin-binding protein 2X [Streptococcus pne	1318	0.0	
dbj BAD00938.1 penicillin-binding protein 2X [Streptococcus pne	1316	0.0	
dbj BAD00922.1 penicillin-binding protein 2X [Streptococcus pne	1316	0.0	
dbj BAD00925.1 penicillin-binding protein 2X [Streptococcus pne	1315	0.0	
dbj BAD00926.1 penicillin-binding protein 2X [Streptococcus pne	1315	0.0	
gb AAF17268.1 AF210758_1 penicillin-binding protein 2X [Streptoc	1313	0.0	
gb AAF17270.1 AF210760_1 penicillin-binding protein 2X [Streptoc	1312	0.0	
dbj BAD00932.1 penicillin-binding protein 2X [Streptococcus pne	1312	0.0	
gb AAF17269.1 AF210759_1 penicillin-binding protein 2X [Streptoc	1312	0.0	
dbj BAD00936.1 penicillin-binding protein 2X [Streptococcus pne	1312	0.0	
gb AAL77081.1 AF468152_1 penicillin-binding protein 2X [Streptoc	1307	0.0	
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dbj BAD00935.1 penicillin-binding protein 2X [Streptococcus pne	1306	0.0	
dbj BAD00906.1 penicillin-binding protein 2X [Streptococcus pne	1305	0.0	
dbj BAD00937.1 penicillin-binding protein 2X [Streptococcus pne	1303	0.0	
pdb 1RP5 A Chain A, Pbp2x From Streptococcus Pneumoniae Strai...	1297	0.0	S
dbj BAD00914.1 penicillin-binding protein 2X [Streptococcus ...	1296	0.0	
dbj BAD00928.1 penicillin-binding protein 2X [Streptococcus pne	1294	0.0	
pdb 1PMD Chain , Penicillin-Binding Protein 2x (Pbp-2x)	1294	0.0	
gb AAC45547.1 low-affinity penicillin-binding protein 2X [St...	1284	0.0	
dbj BAD00915.1 penicillin-binding protein 2X [Streptococcus pne	1279	0.0	
dbj BAD00940.1 penicillin-binding protein 2X [Streptococcus pne	1275	0.0	
gb AY56845.1 penicillin-binding protein 2X [Streptococcus pneu	1271	0.0	
dbj BAD00908.1 penicillin-binding protein 2X [Streptococcus ...	1269	0.0	
gb ABB46504.1 penicillin binding protein 2x [Streptococcus p...	1258	0.0	
gb AAN32862.1 penicillin-binding protein 2X [Streptococcus pneu	1235	0.0	
gb AAN32857.1 penicillin-binding protein 2X [Streptococcus p...	1234	0.0	
emb CAB65447.1 penicillin binding protein 2x [Streptococcus pne	1230	0.0	
gb AAN32865.1 penicillin-binding protein 2X [Streptococcus pneu	1222	0.0	
emb CAD90770.1 penicillin-binding protein 2x [Streptococcus pne	1217	0.0	
emb CAD90771.2 penicillin-binding protein 2x [Streptococcus pne	1209	0.0	
gb AY56843.1 penicillin-binding protein 2X [Streptococcus p...	1207	0.0	
gb AY56850.1 penicillin-binding protein 2X [Streptococcus pneu	1206	0.0	
gb AY56847.1 penicillin-binding protein 2X [Streptococcus pneu	1204	0.0	

gb AAV56846.1	penicillin-binding protein 2X [Streptococcus pneu	1198	0.0
-gb AAV56857.1	penicillin-binding protein 2X [Streptococcus pneu	1197	0.0
emb CAB65444.1	penicillin binding protein 2x [Streptococcus pne	1188	0.0
gb AAN32852.1	penicillin-binding protein 2X [Streptococcus p...	1187	0.0
gb AAN32861.1	penicillin-binding protein 2X [Streptococcus pneu	1186	0.0
gb AAN32863.1	penicillin-binding protein 2X [Streptococcus pneu	1183	0.0
pdb 1K25 A	Chain A, Pbp2x From A Highly Penicillin-Resistant ...	1183	0.0
gb ABB46505.1	penicillin binding protein 2x [Streptococcus pneu	1182	0.0
gb ABB46506.1	penicillin binding protein 2x [Streptococcus pneu	1181	0.0
gb AAV56848.1	penicillin-binding protein 2X [Streptococcus pneu	1180	0.0
emb CAB65446.1	penicillin binding protein 2x [Streptococcus pne	1179	0.0
gb AAN32859.1	penicillin-binding protein 2X [Streptococcus pneu	1176	0.0
gb AAV56854.1	penicillin-binding protein 2X [Streptococcus pneu	1174	0.0
gb AAN32860.1	penicillin-binding protein 2X [Streptococcus pneu	1174	0.0
gb AAV56839.1	penicillin-binding protein 2X [Streptococcus pneu	1170	0.0
emb CAB65445.1	penicillin binding protein 2x [Streptococcus pne	1170	0.0
emb CAA67013.1	penicillin-binding protein [Streptococcus pneumo	1169	0.0
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emb CAB65441.1	penicillin binding protein 2x [Streptococcus pne	1157	0.0
gb AAN32855.1	penicillin-binding protein 2X [Streptococcus pneu	1157	0.0
gb AAV56849.1	penicillin-binding protein 2X [Streptococcus pneu	1155	0.0
gb AAV56851.1	penicillin-binding protein 2X [Streptococcus pneu	1152	0.0
gb AAV56841.1	penicillin-binding protein 2X [Streptococcus pneu	1150	0.0
emb CAA88920.1	penicillin-binding protein 2x [Streptococcus pne	1149	0.0
emb CAA88919.1	penicillin-binding protein 2x [Streptococcus pne	1149	0.0
emb CAB65448.1	penicillin binding protein 2x [Streptococcus pne	1148	0.0
emb CAA67012.1	penicillin-binding protein [Streptococcus pneumo	1148	0.0
emb CAA67010.1	penicillin-binding protein [Streptococcus pneumo	1146	0.0
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gb AAN32864.1	penicillin-binding protein 2X [Streptococcus pneu	1143	0.0
emb CAA67011.1	penicillin-binding protein [Streptococcus pneumo	1141	0.0
gb AAV56840.1	penicillin-binding protein 2X [Streptococcus pneu	1140	0.0
gb AAN32856.1	penicillin-binding protein 2X [Streptococcus pneu	1139	0.0
gb ABB46508.1	penicillin binding protein 2x [Streptococcus pneu	1135	0.0
gb AAV56855.1	penicillin-binding protein 2X [Streptococcus pneu	1135	0.0

S

Alignments

>sp|P59676|PBPX_STRR6 **G** Penicillin-binding protein 2X (PBP-2X) (PBP2X)
Length=750

Score = 1441 bits (3729), Expect = 0.0, Method: Composition-based stats.
Identities = 750/750 (100%), Positives = 750/750 (100%), Gaps = 0/750 (0%)

Query 1	MKWTKRVIKYATKNRKSPAENRRVGKSLSSLGVFAIFLVNFAVIIGTGTGTDLAK MKWTKRVIKYATKNRKSPAENRRVGKSLSSLGVFAIFLVNFAVIIGTGTGTDLAK	60
Sbjct 1	MKWTKRVIKYATKNRKSPAENRRVGKSLSSLGVFAIFLVNFAVIIGTGTGTDLAK	60
Query 61	EAKKVHQTRRTVPAKRGTIYDRNGVPIAEDATSYNVYAVIDENYKSATGKILYVEKTQFN EAKKVHQTRRTVPAKRGTIYDRNGVPIAEDATSYNVYAVIDENYKSATGKILYVEKTQFN	120
Sbjct 61	EAKKVHQTRRTVPAKRGTIYDRNGVPIAEDATSYNVYAVIDENYKSATGKILYVEKTQFN	120
Query 121	KVAEVFHKYLDMEESYVREQLSQPNLKQVSFGAKGNIGHTYANMMSIKKELEAAEVKGIDF KVAEVFHKYLDMEESYVREQLSQPNLKQVSFGAKGNIGHTYANMMSIKKELEAAEVKGIDF	180
Sbjct 121	KVAEVFHKYLDMEESYVREQLSQPNLKQVSFGAKGNIGHTYANMMSIKKELEAAEVKGIDF	180
Query 181	TTSPNRSPNGQFASSFIGLAQLHENEDGSKSLLGTSGMESSLNSILAGTDGIITYEKDR TTSPNRSPNGQFASSFIGLAQLHENEDGSKSLLGTSGMESSLNSILAGTDGIITYEKDR	240
Sbjct 181	TTSPNRSPNGQFASSFIGLAQLHENEDGSKSLLGTSGMESSLNSILAGTDGIITYEKDR	240
Query 241	LGNIVPGTEQVSQRTMDGKDVTIISSPQSFMETQMDAFQEVKVKGKYMATLVSAKTGE LGNIVPGTEQVSQRTMDGKDVTIISSPQSFMETQMDAFQEVKVKGKYMATLVSAKTGE	300
Sbjct 241	LGNIVPGTEQVSQRTMDGKDVTIISSPQSFMETQMDAFQEVKVKGKYMATLVSAKTGE	300
Query 301	ILATTQRPTFDADTKEGITEDFVWRDILYQSNSYEPGSTMKVMMLAAAIDNNNTFPGEVFN ILATTQRPTFDADTKEGITEDFVWRDILYQSNSYEPGSTMKVMMLAAAIDNNNTFPGEVFN	360
Sbjct 301	ILATTQRPTFDADTKEGITEDFVWRDILYQSNSYEPGSTMKVMMLAAAIDNNNTFPGEVFN	360

Query	361	SSELKIADATIRDWDVNEGTLGGRMMTFSQGFAHSSNVGMTLLEQKMGDATWLDYLNRFK	420
Sbjct	361	SSELKIADATIRDWDVNEGTLGGRMMTFSQGFAHSSNVGMTLLEQKMGDATWLDYLNRFK	420
Query	421	FGVPTRFGLTDEYAGQLPADMINVNIAQSSFGQGISVTQTQMIRAFTAIANDGVMLEPKFI	480
Sbjct	421	FGVPTRFGLTDEYAGQLPADMINVNIAQSSFGQGISVTQTQMIRAFTAIANDGVMLEPKFI	480
Query	481	SAIYDPNDQTARKSQKEIVGNPVSKDAASLRTNMVLVGTDPVYGTMYNHSTGKPTVTVP	540
Sbjct	481	SAIYDPNDQTARKSQKEIVGNPVSKDAASLRTNMVLVGTDPVYGTMYNHSTGKPTVTVP	540
Query	541	GQVALKSGTAQIADEKNGGYLVGLTDYIFSAVMSSPAENPDFILYVTVQQPEHYSGIQL	600
Sbjct	541	GQVALKSGTAQIADEKNGGYLVGLTDYIFSAVMSSPAENPDFILYVTVQQPEHYSGIQL	600
Query	601	GEFANPILERASAMKDSLNLQTTAKALEQVSQQSPYPMPSVKDISPGDLAELRRNLVQP	660
Sbjct	601	GEFANPILERASAMKDSLNLQTTAKALEQVSQQSPYPMPSVKDISPGDLAELRRNLVQP	660
Query	661	IVVGTGTKIKNSSAEGKNLAPNQQVLILSDKAEEVPDMYGWTKETAETLAKWLNLIELEF	720
Sbjct	661	IVVGTGTKIKNSSAEGKNLAPNQQVLILSDKAEEVPDMYGWTKETAETLAKWLNLIELEF	720
Query	721	QGSGSTVQKQDVRANTAIKDIKKITLTLD 750	
Sbjct	721	QGSGSTVQKQDVRANTAIKDIKKITLTLD 750	

>dbj|BAD00902.1| penicillin-binding protein 2X [Streptococcus pneumoniae]
Length=750

Score = 1439 bits (3726), Expect = 0.0, Method: Composition-based stats.
Identities = 749/750 (99%), Positives = 749/750 (99%), Gaps = 0/750 (0%)
Query 1 MKWTKRVIRYATKNRKPSPAEENRRVGKSLSSLGVFAIFLVNFAVIIGTGTRFGTDLAK 60
Sbjct 1 MKWTKRVIRYATKNRKPSPAEENRRVGKSLSSLGVFAIFLVNFAVIIGTGTRFGTDLAK 60
Query 61 EAKKVHQTTRTVPAKRGTIYDRNGVPIAÉDATSYNVYAVIDENYKSATGKILYVEKTQFN 120
Sbjct 61 EAKKVHQTTRTVPAKRGTIYDRNGVPIAEDATSYNVYAVIDENYKSATGKILYVEKTQFN 120
Query 121 KVAEVFHKYLDMEESYVREQLSQPNLKQVSFGAKGNIGHTANMMSIKKELEAAEVKGIDF 180
Sbjct 121 KVAEVFHKYLDMEESYVREQLSQPNLKQVSFGAKGNIGHTANMMSIKKELEAAEVKGIDF 180
Query 181 TTSPNRSPNGQFASSFIGLAQLHENEDEGSKSLLGTSGMESSLNSILAGTDGIITYEKDR 240
Sbjct 181 TTSPNRSPNGQFASSFIGLAQLHENEDEGSKSLLGTSGMESSLNSILAGTDGIITYEKDR 240
Query 241 LGNIVPGTEQVSQRTMDGKDVTIISPLQSFMETQMDAFQEVKVKGKYMATLVSAKTGE 300
Sbjct 241 LGNIVPGTEQVSQRTMDGKDVTIISPLQSFMETQMDAFQEVKVKGKYMATLVSAKTGE 300
Query 301 ILATTQRPTFDADTKEGITEDFVWRDILYQSNYEPGSTMVKVMMAAAIDNNTFPGGEVFN 360
Sbjct 301 ILATTQRPTFDADTKEGITEDFVWRDILYQSNYEPGSTMVKVMMAAAIDNNTFPGGEVFN 360
Query 361 SSELKIADATIRDWDVNEGTLGGRMMTFSQGFAHSSNVGMTLLEQKMGDATWLDYLNRFK 420
Sbjct 361 SSELKIADATIRDWDVNEGTLGGRMMTFSQGFAHSSNVGMTLLEQKMGDATWLDYLNRFK 420
Query 421 FGVPTRFGLTDEYAGQLPADMINVNIAQSSFGQGISVTQTQMIRAFTAIANDGVMLEPKFI 480
Sbjct 421 FGVPTRFGLTDEYAGQLPADMINVNIAQSSFGQGISVTQTQMIRAFTAIANDGVMLEPKFI 480
Query 481 SAIYDPNDQTARKSQKEIVGNPVSKDAASLRTNMVLVGTDPVYGTMYNHSTGKPTVTVP 540
Sbjct 481 SAIYDPNDQTARKSQKEIVGNPVSKDAASLRTNMVLVGTDPVYGTMYNHSTGKPTVTVP 540
Query 541 GQVALKSGTAQIADEKNGGYLVGLTDYIFSAVMSSPAENPDFILYVTVQQPEHYSGIQL 600
Sbjct 541 GQVALKSGTAQIADEKNGGYLVGLTDYIFSAVMSSPAENPDFILYVTVQQPEHYSGIQL 600
Query 601 GEFANPILERASAMKDSLNLQTTAKALEQVSQQSPYPMPSVKDISPGDLAELRRNLVQP 660
Sbjct 601 GEFANPILERASAMKDSLNLQTTAKALEQVSQQSPYPMPSVKDISPGDLAELRRNLVQP 660
Query 661 IVVGTGTKIKNSSAEGKNLAPNQQVLILSDKAEEVPDMYGWTKETAETLAKWLNLIELEF 720
Sbjct 661 IVVGTGTKIKNSSAEGKNLAPNQQVLILSDKAEEVPDMYGWTKETAETLAKWLNLIELEF 720
Query 721 QGSGSTVQKQDVRANTAIKDIKKITLTLD 750
Sbjct 721 QGSGSTVQKQDVRANTAIKDIKKITLTLD

Sbjct 721 QGSGSTVQKQDVRANTAIKDIKKITLTLGD 750

>dbj|BAD67448.1| penicillin-binding protein 2X [Streptococcus pneumoniae]
Length=750Score = 1438 bits (3723), Expect = 0.0, Method: Composition-based stats.
Identities = 748/750 (99%), Positives = 748/750 (99%), Gaps = 0/750 (0%)

Query 1	MKWTKR VIRYAT KNRK SPAEN RRRVGKS LLS SVF VFAI F L VNFA I IGTGTRG TD LAK	60
Sbjct 1	MKWTKR VIRYAT KNRK SPAEN RRRVGKS LLS SVF VFAI F L VNFA I IGTGTRG TD LAK	60
Query 61	EAKKVHQ TTRTVP AKRG TI YDRNGVPIAEDATSY NVYAVIDENYKSATGKILYVEKTQFN	120
Sbjct 61	EAKKVHQ TTRTVP AKRG TI YDRNGVPIAEDATSY NVYAVIDENYKSATGKILYVEKTQFN	120
Query 121	KVAEVFH KYLDMEESYVREQLSQPNLKQVSFGAKGN GITYANMMSIKKELEAAEVKGIDF	180
Sbjct 121	KVAEVFH KYLDMEESYVREQLSQPNLKQVSFGAKGN GITYANMMSIKKELEAAEVKGIDF	180
Query 181	TTSPNRSYPNGQFASSFIGLAQLHENE DGSKSLLGTSGMESSLNSILAGTDGIITYEKDR	240
Sbjct 181	TTSPNRSYPNGQFASSFIGLAQLHENE DGSKSLLGTSGMESSLNSILAGTDGIITYEKDR	240
Query 241	LGNIVPGTEQV SQRTMDGKD VYTTI SSSPLQS FMETQMDAFQEKVKGKYM TATL VS A KTG E	300
Sbjct 241	LGNIVPGTEQV SQRTMDGKD VYTTI SSSPLQS FMETQMDAFQEKVKGKYM TATL VS A KTG E	300
Query 301	I LAT TQRPTFDADTK EG I T EDFW WRD I LYQ S NYEPG STM KVMM LAAA IDN NTF PGGEV FN	360
Sbjct 301	I LAT TQRPTFDADTK EG I T EDFW WRD I LYQ S NYEPG STM KVMM LAAA IDN NTF PGGEV FN	360
Query 361	SSELKIADATI RDWDVNEGLTGRMM TFSQGFAHSSNVGM TLLEQKMGDATWLDYLNR FK	420
Sbjct 361	SSELKIADATI RDWDVNEGLTGRMM TFSQGFAHSSNVGM TLLEQKMGDATWLDYLNR FK	420
Query 421	FGVPTRFGLTDEYAGQLPADNIVNIAQSSFGQG I SVTQTQ MIR AFTAI ANDGV MLEPKFI	480
Sbjct 421	FGVPTRFGLTDEYAGQLPADNIVNIAQSSFGQG I SVTQTQ MIR AFTAI ANDGV MLEPKFI	480
Query 481	SAIYDPNDQTARKS QKEIVGNP VSKDAASL RTNMVLVGTDPVY GTM NHSTGKPTVTVP	540
Sbjct 481	SAIYDPNDQTARKS QKEIVGNP VSKDAASL RTNMVLVGTDPVY GTM NHSTGKPTVTVP	540
Query 541	GQVALKSGTAQIADEKNGGYLVGLTDY I FSAVMSPAENPDFI LYVTVQ QPEH YSGIQL	600
Sbjct 541	GQVALKSGTAQIADEKNGGYLVGLTDY I FSAVMSPAENPDFI LYVTVQ QPEH YSGIQL	600
Query 601	GEFANPI LERASAMKDSLNLQTTAKALEQV SQSPYPMPSV KDISPGD LAEELRRN L VQP	660
Sbjct 601	GEFANPI LERASAMKDSLNLQTTAKALEQV SQSPYPMPSV KDISPGD LAEELRRN L VQP	660
Query 661	I VVGTGKIKNSSAEEGKNLAPN QV L L S DKAEE VPDMY GWT KETAETLAKWL NIELE F	720
Sbjct 661	I VVGTGKIKNSSAEEGKNLAPN QV L L S DKAEE VPDMY GWT KETAETLAKWL NIELE F	720
Query 721	QGSGSTVQKQDVRANTAIKDIKKITLTLGD 750	
Sbjct 721	QGSGSTVQKQDVRANTAIKDIKKITLTLGD 750	

>sp|P14677|PBPX_STRPN Penicillin-binding protein 2x (PBP-2x) (PBP2x)
Length=750Score = 1438 bits (3723), Expect = 0.0, Method: Composition-based stats.
Identities = 749/750 (99%), Positives = 749/750 (99%), Gaps = 0/750 (0%)

Query 1	MKWTKR VIRYAT KNRK SPAEN RRRVGKS LLS SVF VFAI F L VNFA I IGTGTRG TD LAK	60
Sbjct 1	MKWTKR VIRYAT KNRK SPAEN RRRVGKS LLS SVF VFAI F L VNFA I IGTGTRG TD LAK	60
Query 61	EAKKVHQ TTRTVP AKRG TI YDRNGVPIAEDATSY NVYAVIDENYKSATGKILYVEKTQFN	120
Sbjct 61	EAKKVHQ TTRTVP AKRG TI YDRNGVPIAEDATSY NVYAVIDENYKSATGKILYVEKTQFN	120
Query 121	KVAEVFH KYLDMEESYVREQLSQPNLKQVSFGAKGN GITYANMMSIKKELEAAEVKGIDF	180
Sbjct 121	KVAEVFH KYLDMEESYVREQLSQPNLKQVSFGAKGN GITYANMMSIKKELEAAEVKGIDF	180
Query 181	TTSPNRSYPNGQFASSFIGLAQLHENE DGSKSLLGTSGMESSLNSILAGTDGIITYEKDR	240
Sbjct 181	TTSPNRSYPNGQFASSFIGLAQLHENE DGSKSLLGTSGMESSLNSILAGTDGIITYEKDR	240
Query 241	LGNIVPGTEQV SQRTMDGKD VYTTI SSSPLQS FMETQMDAFQEKVKGKYM TATL VS A KTG E	300

Sbjct	241	LGNIVPGTEQVSQRTMDGKDVTIISPLQSFMETQMDAFQEKVKGKYMTATLVSAKTGE	300
Query	301	ILATTQRPTFDADTKEGITEDFWRDILYQSNYEPGSTMVKVMMAAAIDNNTFPGGEVFN	360
Sbjct	301	ILATTQRPTFDADTKEGITEDFWRDILYQSNYEPGSTMVKVMMAAAIDNNTFPGGEVFN	360
Query	361	SSELKIADATIRDWDVNEGLTGRMMTFSQGFAHSSNVGMTLLEQKMGDATWLDYLNRFK	420
Sbjct	361	SSELKIADATIRDWDVNEGLTGRMMTFSQGFAHSSNVGMTLLEQKMGDATWLDYLNRFK	420
Query	421	FGVPTRFLTDEYAGQLPADNIVNIAQSSFGQGISVTQTMIRAFTAIANDGVMLEPKFI	480
Sbjct	421	FGVPTRFLTDEYAGQLPADNIVNIAQSSFGQGISVTQTMIRAFTAIANDGVMLEPKFI	480
Query	481	SAIYDPNDQTARKSQKEIVGNPVSCKDAASLRTNMVLVGTDPVYGTMYNHSTGKPTVTVP	540
Sbjct	481	SAIYDPNDQTARKSQKEIVGNPVSCKDAASLRTNMVLVGTDPVYGTMYNHSTGKPTVTVP	540
Query	541	GQVALKSGTAQIADEKNGGYLVGLTDYIFSAVMSSPAENPDFILYTVQQPEHYSGIQL	600
Sbjct	541	GQVALKSGTAQIADEKNGGYLVGLTDYIFSAVMSSPAENPDFILYTVQQPEHYSGIQL	600
Query	601	GEFANPILERASAMKDSLNLOTTAKALEQVSQQSPYPPMSVKDISPGDLAELRRNLVQP	660
Sbjct	601	GEFANPILERASAMKDSLNLOTTAKALEQVSQQSPYPPMSVKDISPGDLAELRRNLVQP	660
Query	661	IVVGTGKIKNSSAEGKNLAPNQQVLILSDKAEEVPDMYWTKETAETLAKWLNLIELEF	720
Sbjct	661	IVVGTGKIKNSSAEGKNLAPNQQVLILSDKAEEVPDMYWTKETAETLAKWLNLIELEF	720
Query	721	QGSGSTVQKQDVRANTAIKDIKKITLTLGD 750	
Sbjct	721	QGSGSTVQKQDVRANTAIKDIKKITLTLGD 750	

>dbj|BAD00901.1| penicillin-binding protein 2X [Streptococcus pneumoniae]
Length=750

Score = 1438 bits (3722), Expect = 0.0, Method: Composition-based stats.
Identities = 748/750 (99%), Positives = 749/750 (99%), Gaps = 0/750 (0%)

Query	1	MKWTKRVIYATKNRKPSPAEENRRVGKSLSLLSVFVFAIFLVNFAVIIGTGTRGTDLAK	60
Sbjct	1	MKWTKRVIYATKNRKPSPAEENRRVGKSLSLLSVFVFAIFLVNFAVIIGTGTRGTDLAK	60
Query	61	EAKKVHQTRRTVPAKRGTIYDRNGVPIAEDATSYNVYAVIDENYKSATGKILYVEKTQFN	120
Sbjct	61	EAKKVHQTRRTVPAKRGTIYDRNGVPIAEDATSYNVYAVIDENYKSATGKILYVEKTQFN	120
Query	121	KVAEVFKYLDMEESYVREQLSQPNLKQVSFGAKGNIGINANMMSIKKELEAAEVKGIDF	180
Sbjct	121	KVAEVFKYLDMEESYVREQLSQPNLKQVSFGAKGNIGINANMMSIKKELEAAEVKGIDF	180
Query	181	TTSPNRSPNGQFASSFIGLAQLHENEDGSKSLLGTSGMESSLNSILAGTDGIITYEKDR	240
Sbjct	181	TTSPNRSPNGQFASSFIGLAQLHENEDGSKSLLGTSGMESSLNSILAGTDGIITYEKDR	240
Query	241	LGNIVPGTEQVSQRTMDGKDVTIISPLQSFMETQMDAFQEKVKGKYMTATLVSAKTGE	300
Sbjct	241	LGNIVPGTEQVSQRTMDGKDVTIISPLQSFMETQMDAFQEKVKGKYMTATLVSAKTGE	300
Query	301	ILATTQRPTFDADTKEGITEDFWRDILYQSNYEPGSTMVKVMMAAAIDNNTFPGGEVFN	360
Sbjct	301	ILATTQRPTFDADTKEGITEDFWRDILYQSNYEPGSTMVKVMMAAAIDNNTFPGGEVFN	360
Query	361	SSELKIADATIRDWDVNEGLTGRMMTFSQGFAHSSNVGMTLLEQKMGDATWLDYLNRFK	420
Sbjct	361	SSELKIADATIRDWDVNEGLTGRMMTFSQGFAHSSNVGMTLLEQKMGDATWLDYLNRFK	420
Query	421	FGVPTRFLTDEYAGQLPADNIVNIAQSSFGQGISVTQTMIRAFTAIANDGVMLEPKFI	480
Sbjct	421	FGVPTRFLTDEYAGQLPADNIVNIAQSSFGQGISVTQTMIRAFTAIANDGVMLEPKFI	480
Query	481	SAIYDPNDQTARKSQKEIVGNPVSCKDAASLRTNMVLVGTDPVYGTMYNHSTGKPTVTVP	540
Sbjct	481	SAIYDPNDQTARKSQKEIVGNPVSCKDAASLRTNMVLVGTDPVYGTMYNHSTGKPTVTVP	540
Query	541	GQVALKSGTAQIADEKNGGYLVGLTDYIFSAVMSSPAENPDFILYTVQQPEHYSGIQL	600
Sbjct	541	GQVALKSGTAQIADEKNGGYLVGLTDYIFSAVMSSPAENPDFILYTVQQPEHYSGIQL	600
Query	601	GEFANPILERASAMKDSLNLOTTAKALEQVSQQSPYPPMSVKDISPGDLAELRRNLVQP	660
Sbjct	601	GEFANPILERASAMKDSLNLOTTAKALEQVSQQSPYPPMSVKDISPGDLAELRRNLVQP	660
Query	661	IVVGTGKIKNSSAEGKNLAPNQQVLILSDKAEEVPDMYWTKETAETLAKWLNLIELEF	720

Sbjct	661	IVVGTGKIKNSSAEEGKNLAPNQQVLILSDK EEVPDMDYGTWTKETAETLAKWLNLIELEF	720
Query	721	QSGGSTVQKQDVRANTAIKDIKKITLTD 750	
Sbjct	721	QSGGSTVQKQDVRANTAIKDIKKITLTD 750	

>dbj|BAD00904.1| penicillin-binding protein 2X [Streptococcus pneumoniae]
Length=750

Score = 1436 bits (3718), Expect = 0.0, Method: Composition-based stats.
Identities = 748/750 (99%), Positives = 749/750 (99%), Gaps = 0/750 (0%)

Query	1	MKWTKRVIKYATKNRKSPAENRRVGKSLSSLSSVFAIFLVNFAVIIGTGTRFGTDLAK	60
Sbjct	1	MKWTKRVIKYATKNRKSPAENRRVGKSLSSLSSVFAIFLVNFAVIIGTGTRFGTDLAK	60
Query	61	EAKKVHQTRTVPAKRGTIYDRNGVPIAEDATSYNVYAVIDENYKSATGKILYVEKTQFN	120
Sbjct	61	EAKKVHQTRTVPAKRGTIYDRNGVPIAEDATSYNVYAVIDENYKSATGKILYVEKTQFN	120
Query	121	KVAEVFKYLDMEESYVREQLSQPNLKQVSFGAKGNNGITYANMMSIKKELEAAEVKGIDF	180
Sbjct	121	KVAEVFKYLDMEESYVREQLSQPNLKQVSFGAKGNNGITYANMMSIKKELEAAEVKGIDF	180
Query	181	TTSPNRSPNGQFASSFIGLAQLHENEDGSKSLLGTSGMESSLNSILAGTDGIITYEKDR	240
Sbjct	181	TTSPNRSPNGQFASSFIGLAQLHENEDGSKSLLGTSGMESSLNSILAGTDGIITYEKDR	240
Query	241	LGNIVPGTEQVSQRTMDGKDVTIISPLQSFMETQMDAFQEVKVKGKYMATLVSAKTGE	300
Sbjct	241	LGNIVPGTEQVSQRTMDGKDVTIISPLQSFMETQMDAFQEVKVKGKYMATLVSAKTGE	300
Query	301	ILATTQRPTFDADTKEGITEDFWRDILYQSNYEPGSTMVKVMMAAAIDNNTFPGGEVFN	360
Sbjct	301	ILATTQRPTFDADTKEGITEDFWRDILYQSNYEPGSTMVKVMMAAAIDNNTFPGGEVFN	360
Query	361	SSELKIADATIRDWDVNEGLTGGRRMMTSQGFAHSSNVGMTLLEQKMGDATWLDYLNRFK	420
Sbjct	361	SSELKIADATIRDWDVNEGLTGGRRMMTSQGFAHSSNVGMTLLEQKMGDATWLDYLNRFK	420
Query	421	FGVPTRFGLTDEYAGQLPADNIVNIAQSSFGQGISVTQTQMIRAFTAIANDGVMLEPKFI	480
Sbjct	421	FGVPTRFGLTDEYAGQLPADNIVNIAQSSFGQGISVTQTQMIRAFTAIANDGVMLEPKFI	480
Query	481	SAIYDPNDQTARKSQKEIVGNPVSCKDAASLRTNMVLVGTDPVYGTMYNSTGKPTVTVP	540
Sbjct	481	SAIYDPNDQTARKSQKEIVGNPVSCKDAASLRTNMVLVGTDPVYGTMYNSTGKPTVTVP	540
Query	541	GQVALKSGTAQIADEKNGGYLVGLTDYIFSAVMSSPAENPDFILYTVQOPEHYSGIQL	600
Sbjct	541	GQVALKSGTAQIADEKNGGYLVG+TDYIFSAVMSSPAENPDFILYTVQOPEHYSGIQL	600
Query	601	GEFANPILEASAMKDSLNLTQTTAKALEQVSQQSPYPMPSVKDISPGDLAELRRNLVQP	660
Sbjct	601	EEFANPILEASAMKDSLNLTQTTAKALEQVSQQSPYPMPSVKDISPGDLAELRRNLVQP	660
Query	661	IVVGTGKIKNSSAEEGKNLAPNQQVLILSDKAEVVPDMYGTWTKETAETLAKWLNLIELEF	720
Sbjct	661	IVVGTGKIKNSSAEEGKNLAPNQQVLILSDKAEVVPDMYGTWTKETAETLAKWLNLIELEF	720
Query	721	QSGGSTVQKQDVRANTAIKDIKKITLTD 750	
Sbjct	721	QSGGSTVQKQDVRANTAIKDIKKITLTD 750	

>gb|AAF17263.1|AF210753_1 penicillin-binding protein 2X [Streptococcus pneumoniae]
Length=750

Score = 1434 bits (3713), Expect = 0.0, Method: Composition-based stats.
Identities = 747/750 (99%), Positives = 748/750 (99%), Gaps = 0/750 (0%)

Query	1	MKWTKRVIKYATKNRKSPAENRRVGKSLSSLSSVFAIFLVNFAVIIGTGTRFGTDLAK	60
Sbjct	1	MKWTKRVIKYATKNRKSPAENRRVGKSLSSLSSVFAIFLVNFAVIIGTGTRFGTDLAK	60
Query	61	EAKKVHQTRTVPAKRGTIYDRNGVPIAEDATSYNVYAVIDENYKSATGKILYVEKTQFN	120
Sbjct	61	EAKKVHQTRTVPAKRGTIYDRNGVPIAEDATSYNVYAVIDENYKSATGKILYVEKTQFN	120
Query	121	KVAEVFKYLDMEESYVREQLSQPNLKQVSFGAKGNNGITYANMMSIKKELEAAEVKGIDF	180
Sbjct	121	KVAEVFKYLDMEESYVREQLSQPNLKQVSFGAKGNNGITYANMMSIKKELEAAEVKGIDF	180
Query	181	TTSPNRSPNGQFASSFIGLAQLHENEDGSKSLLGTSGMESSLNSILAGTDGIITYEKDR	240

Sbjct	181	TTSPNRSPNGQFASSFIGLAQLHENEDGSKSLLGTSGMESSLNSILAGTDGIITYEKDR TTSPNRSPNGQFASSFIGLAQLHENEDGSKSLLGTSGMESSLNSILAGTDGIITYEKDR	240
Query	241	LGNIVPGTEQVSQRTMDGKDVTYTTISSLQSFMETQMDAFQEKVKGKYMATLVSAKTGE LGNIVPGTEQVSQRTMDGKDVTYTTISSLQSFMETQMDAFQEKVKGKYMATLVSAKTGE	300
Sbjct	241	LGNIVPGTEQVSQRTMDGKDVTYTTISSLQSFMETQMDAFQEKVKGKYMATLVSAKTGE LGNIVPGTEQVSQRTMDGKDVTYTTISSLQSFMETQMDAFQEKVKGKYMATLVSAKTGE	300
Query	301	ILATTQRPTFDADTKEGITEDFVWRDILYQSNYEPGSTMVKVMMLAAAIDNNTFPGEVFN ILATTQRPTFDADTKEGITEDFVWRDILYQSNYEPGSTMVKVMMLAAAIDNNTFPGEVFN	360
Sbjct	301	ILATTQRPTFDADTKEGITEDFVWRDILYQSNYEPGSTMVKVMMLAAAIDNNTFPGEVFN ILATTQRPTFDADTKEGITEDFVWRDILYQSNYEPGSTMVKVMMLAAAIDNNTFPGEVFN	360
Query	361	SSELKIADATIRDWVNNEGLTGGRMMTFSQGFAHSSNVGMTLLEQKMGDATWLDYLNRFK SSELKIADATIRDWVNNEGLTGGRMMTFSQGFAHSSNVGMTLLEQKMGDATWLDYLNRFK	420
Sbjct	361	SSELKIADATIRDWVNNEGLTGGRMMTFSQGFAHSSNVGMTLLEQKMGDATWLDYLNRFK SSELKIADATIRDWVNNEGLTGGRMMTFSQGFAHSSNVGMTLLEQKMGDATWLDYLNRFK	420
Query	421	FGVPTRFGLTDEYAGQLPADNIVNIAQSSFGQGISVTQTQMIRAFTAIANDGVMLEPKFI FGVPTRFGLTDEYAGQLPADNIVNIAQSSFGQGISVTQTQMIRAFTAIANDGVMLEPKFI	480
Sbjct	421	FGVPTRFGLTDEYAGQLPADNIVNIAQSSFGQGISVTQTQMIRAFTAIANDGVMLEPKFI FGVPTRFGLTDEYAGQLPADNIVNIAQSSFGQGISVTQTQMIRAFTAIANDGVMLEPKFI	480
Query	481	SAIYDPNDQTARKSQKEIVGNPVSKDAASLRTTNMVLVGTDPVYGTMYNHSTGKPTVTVP SAIYDPNDQTARKSQKEIVGNPVSKDAASLRTTNMVLVGTDPVYGTMYNHSTGKPTVTVP	540
Sbjct	481	SAIYDPNDQTARKSQKEIVGNPVSKDAASLRTTNMVLVGTDPVYGTMYNHSTGKPTVTVP SAIYDPNDQTARKSQKEIVGNPVSKDAASLRTTNMVLVGTDPVYGTMYNHSTGKPTVTVP	540
Query	541	GQNVALKSGTAQIADEKNGGYLVGLTDYIFSAVSMSPAENPDFILYVTVQQPEHYSGIQL GQNVALKSGTAQIADEKNGGYLVG+TDYIFSAVSMSPAENPDFILYVTVQQPEHYSGIQL	600
Sbjct	541	GQNVALKSGTAQIADEKNGGYLVGVTDYIFSAVSMSPAENPDFILYVTVQQPEHYSGIQL GQNVALKSGTAQIADEKNGGYLVGVTDYIFSAVSMSPAENPDFILYVTVQQPEHYSGIQL	600
Query	601	GEFANPILERASAMKDSLNLQTTAKALEQVSQQSPYPMPSVKDISPGDLAELRRNLVQP GEFANPILERASAMKDSLNLQTTAKALEQVSQQSPYPMPSVKDISPGDLAELRRNLVQP	660
Sbjct	601	GEFANPILERASAMKDSLNLQTTAKALEQVSQQSPYPMPSVKDISPGDLAELRRNLVQP GEFANPILERASAMKDSLNLQTTAKALEQVSQQSPYPMPSVKDISPGDLAELRRNLVQP	660
Query	661	IVVGTGTKIKNSSAEEGKNLAPNQQVLILSDKAAEVPDMYGWTKETAETLAKWLNLIELEF IVVGTGTKIKNSSAEEGKNLAPNQQVLILSDKAAEVPDMYGWTKETAETLAKWLNLIELEF	720
Sbjct	661	IVVGTGTKIKNSSAEEGKNLAPNQQVLILSDKAAEVPDMYGWTKETAETLAKWLNLIELEF IVVGTGTKIKNSSAEEGKNLAPNQQVLILSDKAAEVPDMYGWTKETAETLAKWLNLIELEF	720
Query	721	QGSGSTVQKQDVRANTAIKDIKKITLTLGD 750 QGSGSTVQKQDVRANTAIKDIKKITLTLGD	750
Sbjct	721	QGSGSTVQKQDVRANTAIKDIKKITLTLGD 750 QGSGSTVQKQDVRANTAIKDIKKITLTLGD	750

>dbj|BAD00905.1| penicillin-binding protein 2X [Streptococcus pneumoniae]
dbj|BAD00921.1| penicillin-binding protein 2X [Streptococcus pneumoniae]
Length=750

Score = 1418 bits (3670), Expect = 0.0, Method: Composition-based stats.
Identities = 737/750 (98%), Positives = 745/750 (99%), Gaps = 0/750 (0%)

Query	1	MKWTKRVIYATKNRKSPAENRRVGKSLSSLGVFAIFLVNFAVIIGTGTFRGTDLAK MKWTKRVIYATKNRKSPAENRRVGKSLSSLGVFAIFLVNFAVIIGTGTFRGTDLAK	60
Sbjct	1	MKWTKRVIYATKNRKSPAENRRVGKSLSSLGVFAIFLVNFAVIIGTGTFRGTDLAK MKWTKRVIYATKNRKSPAENRRVGKSLSSLGVFAIFLVNFAVIIGTGTFRGTDLAK	60
Query	61	EAKKVHQTTRTVPAKRGTIYDRNGVPIAEDATSYNVYAVIDENYKSATGKILYVEKTQFN EAKKVHQTTRTVPAKRGTIYDRNGVPIAEDATSYNVYAVIDENYKSATGKILYVEKTQFN	120
Sbjct	61	EAKKVHQTTRTVPAKRGTIYDRNGVPIAEDATSYNVYAVIDENYKSATGKILYVEKTQFN EAKKVHQTTRTVPAKRGTIYDRNGVPIAEDATSYNVYAVIDENYKSATGKILYVEKTQFN	120
Query	121	KVAEVFKYLDMEESYVREQLSQPNLKQVSFGAKGNIGITYANMMSIKKELEAAEVKGIDF KVAEVFKYLDMEESYVREQLSQPNLKQVSFGAKGNIGITYANMMSIKKELEAAEVKGIDF	180
Sbjct	121	KVAEVFKYLDMEESYVREQLSQPNLKQVSFGAKGNIGITYANMMSIKKELEAAEVKGIDF KVAEVFKYLDMEESYVREQLSQPNLKQVSFGAKGNIGITYANMMSIKKELEAAEVKGIDF	180
Query	181	TTSPNRSPNGQFASSFIGLAQLHENEDGSKSLLGTSGMESSLNSILAGTDGIITYEKDR TTSPNRSPNGQFASSFIGLAQLHENEDGSKSLLGTSGMESSLNSILAGTDGIITYEKDR	240
Sbjct	181	TTSPNRSPNGQFASSFIGLAQLHENEDGSKSLLGTSGMESSLNSILAGTDGIITYEKDR TTSPNRSPNGQFASSFIGLAQLHENEDGSKSLLGTSGMESSLNSILAGTDGIITYEKDR	240
Query	241	LGNIVPGTEQVSQRTMDGKDVTYTTISSLQSFMETQMDAFQEKVKGKYMATLVSAKTGE LGNIVPGTEQVSQ+T+DGKDVTYTTISSLQSFMETQMDAFQEKVKGKYMATLVSAKTGE	300
Sbjct	241	LGNIVPGTEQVSQQTVDGKDVTYTTISSLQSFMETQMDAFQEKVKGKYMATLVSAKTGE LGNIVPGTEQVSQQTVDGKDVTYTTISSLQSFMETQMDAFQEKVKGKYMATLVSAKTGE	300
Query	301	ILATTQRPTFDADTKEGITEDFVWRDILYQSNYEPGSTMVKVMMLAAAIDNNTFPGEVFN ILATTQRPTFDADTKEG+T+DFVWRDILYQSNYEPGSTMVKM LAAAIDNNTFPGEVF+	360
Sbjct	301	ILATTQRPTFDADTKEGLTDFVWRDILYQSNYEPGSTMVKM LAAAIDNNTFPGEVF ILATTQRPTFDADTKEGLTDFVWRDILYQSNYEPGSTMVKM LAAAIDNNTFPGEVF	360
Query	361	SSELKIADATIRDWVNNEGLTGGRMMTFSQGFAHSSNVGMTLLEQKMGDATWLDYLNRFK SSELKIAD TIRDWDVNNEGLTGGRMMT SQGFA SSVGMTLLEQKMGDATWLDYLNRFK	420
Sbjct	361	SSELKIAD TIRDWDVNNEGLTGGRMMT LSQGFALSSNVGMTLLEQKMGDATWLDYLNRFK SSELKIAD TIRDWDVNNEGLTGGRMMT LSQGFALSSNVGMTLLEQKMGDATWLDYLNRFK	420
Query	421	FGVPTRFGLTDEYAGQLPADNIVNIAQSSFGQGISVTQTQMIRAFTAIANDGVMLEPKFI FGVPTRFGLTDEYAGQLPADNIVNIAQSSFGQGISVTQTQMIRAFTAIANDGVMLEPKFI	480
Sbjct	421	FGVPTRFGLTDEYAGQLPADNIVNIAQSSFGQGISVTQTQMIRAFTAIANDGVMLEPKFI FGVPTRFGLTDEYAGQLPADNIVNIAQSSFGQGISVTQTQMIRAFTAIANDGVMLEPKFI	480
Query	481	SAIYDPNDQTARKSQKEIVGNPVSKDAASLRTTNMVLVGTDPVYGTMYNHSTGKPTVTVP SAIYDPNDQTARKSQKEIVGNPVSKDAASLRTTNMVLVGTDPVYGTMYNHSTGKPTVTVP	540
Sbjct	481	SAIYDPNDQTARKSQKEIVGNPVSKDAASLRTTNMVLVGTDPVYGTMYNHSTGKPTVTVP SAIYDPNDQTARKSQKEIVGNPVSKDAASLRTTNMVLVGTDPVYGTMYNHSTGKPTVTVP	540
Query	541	GQNVALKSGTAQIADEKNGGYLVGLTDYIFSAVSMSPAENPDFILYVTVQQPEHYSGIQL GQNVALKSGTAQIADEKNGGYLVGLTDYIFSAVSMSPAENPDFILYVTVQQPEHYSGIQL	600
Sbjct	541	GQNVALKSGTAQIADEKNGGYLVGLTDYIFSAVSMSPAENPDFILYVTVQQPEHYSGIQL GQNVALKSGTAQIADEKNGGYLVGLTDYIFSAVSMSPAENPDFILYVTVQQPEHYSGIQL	600

Query	601	GEFANPILERASAMKDSLNLQTTAKALEQVSQQSPYPMPSVKDISPGDLAELRRNLVQP	660
Sbjct	601	GEFANPILERASAMKDSLNLQTTAKALEQVSQQSPYPMPSVKDISPGDLAELRRNLVQP	660
Query	661	IVVGTGKIKNSSAEEGKNLAPNQQVLILSDKAEEVPDMYGWTKETAETLAKWLNLIELEF	720
Sbjct	661	IVVGTGKIKNSSAEEGKNLAPNQQVLILSDKAEEVPDMYGWTKETAETLAKWLNLIELEF	720
Query	721	QGSGSTVQKQDVRANTAIKDIKKITLTLGD 750	
Sbjct	721	QGSGSTVQKQDVRANTAIKDIKKITLTLGD 750	

>dbj|BAD00912.1| penicillin-binding protein 2X [Streptococcus pneumoniae]
Length=750

Score = 1415 bits (3662), Expect = 0.0, Method: Composition-based stats.
Identities = 734/750 (97%), Positives = 744/750 (99%), Gaps = 0/750 (0%)

Query	1	MKWTKRVIKYATKNRSPAENRRVGKSLSSLGVFAIFLVNFAVIIGTGTRFGTDLAK	60
Sbjct	1	MKWTKRVIKYATKNRSPAENRRVGKSLSSLGVFA+FLVNFAVIIGTGTRFGTDLAK	60
Query	61	EAKKVHQTTRTVPAKRGTIYDRNGVPIAEADATSYNVYAVIDENYSATGKILYVEKTQFN	120
Sbjct	61	EAKKVHQTTRTVPAKRGTIYDRNGVPIAEADATSYNVYAVIDENYSATGKILYVEKTQFN	120
Query	121	KVAEVFHKYLDMEESYVREQLSQPNLKQVSFGAKGNIGITYANMMSIKKELEAAEVKGIDF	180
Sbjct	121	KVAEVFHKYLDMEESYVREQLSQPNLKQVSFG+KGNIGITYANMMSIKKELE AEVKGIDF	180
Query	181	TTSPNRSPNGQFASSFIGLAQLHENEDGSKSLLTSGMESSLNSILAGTDGIITYEKDR	240
Sbjct	181	TTSPNRSPNGQFASSFIGLAQLHENEDGSKSLLTSGMESSLN ILAGTDGIITYEKDR	240
Query	241	LGNIVPGTEQVSQRTMDGKDVTIISPLQSFMETQMDAFQEKVKGKYMATLVSAKTGE	300
Sbjct	241	LGNIVPGTEQVSQ+T+DGKDVTIISPLQSFMETQMDAFQEKVKGKYMATLVSAKTGE	300
Query	301	ILATTQRPTFDADTKEGITEDFVWRDILYQSNYEPMGSTMVMMIAAAIDNNTFPGGEVFN	360
Sbjct	301	ILATTQRPTFDADTKEGITEDFVWRDILYQSNYEPMGKVMMLAAAIDNNNTFPGGEVFN	360
Query	361	SSELKIADATIRDWDVNEGLTGGRMMTFSQGFAHSSNVGMTLLEQKMGDATWLDYLNRFK	420
Sbjct	361	SSELKIAD TIRDWDVNEGLTGGRMMTFSQGFAHSSNVGMTLLEQKMGDATWLDYLNRFK	420
Query	421	FGVPTRFGLTDEYAGQLPADNIVNIAQSSFGQGISVTQTQMIRAFTAIANDGVMLEPKFI	480
Sbjct	421	FGVPTRFGLTDEYAGQLPADNIVNIAQSSFGQGISVTQTQMIRAFTAIANDGVMLEPKFI	480
Query	481	SAIYDPNDQTARKSQEIVGNPVSCKDAASLTRLTMVLTGDPVYGTMYNHSTGKPTVTVP	540
Sbjct	481	SAIYDPNDQTARKSQEIVGNPVSCKDAAS TRT+MVLVGTDPVYGT+NHSTGKPTVTVP	540
Query	541	GQVALKSGTAQIADEKNGGYLVGLTDYI FSAVSMSPAENPDFILYTVQQPEHYSGIQL	600
Sbjct	541	GQVALKSGTAQIADEKNGGY+G T+IFSAVSM+PAENPDFILYTVQQPEHYSGIQL	600
Query	601	GEFANPILERASAMKDSLNLQTTAKALEQVSQQSPYPMPSVKDISPGDLAELRRNLVQP	660
Sbjct	601	GEFANPILERASAMKDSLNLQTTAKALEQVSQQSPYPMPSVKDISPGDLAELRRNLVQP	660
Query	661	IVVGTGKIKNSSAEEGKNLAPNQQVLILSDKAEEVPDMYGWTKETAETLAKWLNLIELEF	720
Sbjct	661	IVVGTGKIKNSSAEEGKNLAPNQQVLILSDKAEEVPDMYGWTKETAETLAKWLNLIELEF	720
Query	721	QGSGSTVQKQDVRANTAIKDIKKITLTLGD 750	
Sbjct	721	QGSGSTVQKQDVRANTAIKDIKKITLTLGD 750	

>gb|AAF17266.1|AF210756_1 penicillin-binding protein 2X [Streptococcus pneumoniae]
Length=750

Score = 1397 bits (3617), Expect = 0.0, Method: Composition-based stats.
Identities = 725/750 (96%), Positives = 737/750 (98%), Gaps = 0/750 (0%)

Query	1	MKWTKRVIKYATKNRSPAENRRVGKSLSSLGVFAIFLVNFAVIIGTGTRFGTDLAK	60
Sbjct	1	MKWTKRVIKYATKNRSPAENRRVGKSLSSLGVFA+FLVNFAVIIGTGTRFGTDLAK	60
Query	61	EAKKVHQTTRTVPAKRGTIYDRNGVPIAEADATSYNVYAVIDENYSATGKILYVEKTQFN	120
Sbjct	61	EAKKVHQTTRTVPAKRGTIYDRNGVPIAEADATSYNVYAVIDENYSATGKILYVEKTQFN	120

-Query	121	KVAEVFKYLDMEESYVREQLSQPNLKQVSFGAKGNIGITYANMMSIKKELEAAEVKGIDF	180
Sbjct	121	KVAEVFKYLDMEESYVREQLSQPNLKQVSFGAKGNIGITYANMMSIKKELEAAEVKGIDF	180
-Query	181	TTSPNRSPNGQFASSFIGLAQLHENEDGSKSLLGTSGMESSLNSILAGTDGIITYEKDR	240
Sbjct	181	TTSPNRSPNGQFASSFIGLAQLHENEDGSKSLLGTSGMESSLNSILAGTDGIITYEKDR	240
Query	241	LGNIVPGTEQVSQRTMDGKDVTYTTISSLQSFMETQMDAFQEVKVKGKYMATLVSAKTGE	300
Sbjct	241	LGNIVPGTEQVSQRTMDGKDVTYTTISSLQSFMETQMDAFQEVKVKGKYMATLVSAKTGE	300
Query	301	ILATTQRPTFDADTKEGITEDFWRDILYQSNYEPGSTMKVMMIAAAIDNNTFPGEVFN	360
Sbjct	301	ILATTQRPTFDADTKEGITEDFWRDILYQSNYEPGSTMKVMMIAAAIDNNTFPGEVFN	360
Query	361	SSELKIADATIRDWDVNNEGLTGRMMTFSQGFAHSSNVGMTLLEQKMGDATWLDYLNRFK	420
Sbjct	361	SSELKIADATIRDWDVN+GLT G MMTF QGFAHSSNVGM+LLEQKMGDATWLDYLNRFK	420
Query	421	FGVPTRGFLDEYAGQLPADNIVNIAQSSFGQGISVTQTQMIRAFTAIANDGVMLEPKFI	480
Sbjct	421	FGVPTRGFLDEYAGQLPADNIVNIA S+FGQGISVTQTQM+RAFTAIA ANDGVMLEPKFI	480
Query	481	SAIYDPNDQTARKSQEIVGNPVSCKDAASLRTNMVLVGDTPVYGTMYNHSTGKPTVTVP	540
Sbjct	481	SAIYDPNDQTARKSQEIVGNPVSCKDAASLRTNM+LVGDTPVYGTMYNHSTGKPTVTVP	540
Query	541	GQVALKSGTAQIADEKNGGYLVGLTDYIFSAVSMSPAENPDFILYVTVQQPEHYSGIQL	600
Sbjct	541	GQVALKSGTA+IADEKNGGYLVG T+ IFS V+M+ PAENPDFILYVTVQQPEHYSGIQL	600
Query	601	GEFANPILEASAMKDSLNLQTTAKALEQVSQQSPYPMPSVKDISPGDLAEELRRNLVQP	660
Sbjct	601	GEFTNPILERASAMKDSLNLQTTAKALEQVSQQSPYPMPSVKDISPGDLAEELRRNLVQP	660
Query	661	IVVGTGKIKNSSAEEGKNLAPNQQVLILSDKAEEVPDMYGWTKETAETLAKWLNLIELEF	720
Sbjct	661	IVVGTGKIKNSSAEEGKNLAPNQQVLILSDKAEEVPDMYGWTK TAET AKWLNLIELEF	720
Query	721	QGSGSTVQKQDVRANTAIKDIKKITLTG 750	
Sbjct	721	+GSGSTVQKQDVRANTAIKDIKKITLTG 750	
Sbjct	721	EGSGSTVQKQDVRANTAIKDIKKITLTG 750	

>gb|AAF17265.1|AF210755 1 penicillin-binding protein 2X [Streptococcus pneumoniae]
 >gb|AAC95456.1| penicillin-binding protein 2x [Streptococcus pneumoniae]
 Length=750

Score = 1395 bits (3612), Expect = 0.0, Method: Composition-based stats.
 Identities = 723/750 (96%), Positives = 737/750 (98%), Gaps = 0/750 (0%)

Query	1	MKWTKRVIKYATKNRKSPAENRRVGKSLSSLGVFAIFLVNFAVIIGTGTRGTDLAK	60
Sbjct	1	MKWTKRVIKYATKNRKSPAENRRVGKSLSSLGVFAIFLVNFAVIIGTGTRGTDLAK	60
Query	61	EAKKVHQTRRTVPAKRGTIYDRNGVPIAEDATSYNVYAVIDENYKSATGKILYVEKTQFN	120
Sbjct	61	EAKKVHQTRRTVPAKRGTIYDRNGVPIAEDATSYNVYAVIDENYKSATGKILYVEKTQFN	120
Query	121	KVAEVFKYLDMEESYVREQLSQPNLKQVSFGAKGNIGITYANMMSIKKELEAAEVKGIDF	180
Sbjct	121	KVAEVFKYLDMEESYVREQLSQPNLKQVSFGAKGNIGITYANMMSIKKELE AEVKGIDF	180
Query	181	TTSPNRSPNGQFASSFIGLAQLHENEDGSKSLLGTSGMESSLNSILAGTDGIITYEKDR	240
Sbjct	181	TTSPNRSPNGQFASSFIGLAQLHENEDGSKSLLGTSGMESSLNSILAGTDGIITYEKDR	240
Query	241	LGNIVPGTEQVSQRTMDGKDVTYTTISSLQSFMETQMDAFQEVKVKGKYMATLVSAKTGE	300
Sbjct	241	LGNIVPGTEQVSQRTMDGKDVTYTTISSLQSFMETQMDAFQEVKVKGKYMATLVSAKTGE	300
Query	301	ILATTQRPTFDADTKEGITEDFWRDILYQSNYEPGSTMKVMMIAAAIDNNTFPGEVFN	360
Sbjct	301	ILATTQRPTFDADTKEGITEDFWRDILYQSNYEPGSTMKVMMIAAAIDNNTFPGEVFN	360
Query	361	SSELKIADATIRDWDVNNEGLTGRMMTFSQGFAHSSNVGMTLLEQKMGDATWLDYLNRFK	420
Sbjct	361	SSELKIADATIRDWDVNNEGLTGRMMTFSQGFAHSSNVGMTLLEQKMGDATWLDYLNRFK	420
Query	421	FGVPTRGFLDEYAGQLPADNIVNIAQSSFGQGISVTQTQMIRAFTAIANDGVMLEPKFI	480
Sbjct	421	FGVPTRGFLDEYAGQLPADNIVNIA S+FGQGISVTQTQM+RAFTAIA ANDGVMLEPKFI	480
Query	481	SAIYDPNDQTARKSQEIVGNPVSCKDAASLRTNMVLVGDTPVYGTMYNHSTGKPTVTVP	540

- Sbjct	481	SA+YDPNDQ+ RKSQKEIVGNPVSK+AAS+TR +MV+VGTDP YGTMYNHSTGK TV VP SALYDPNDQSVRKSKQKEIVGNPVSKEASVTRDHMVMVGTDPYGTMYNHSTGKATVNVP	540
Query	541	GQVALKSGTAQIADEKNGGYLVGLTDYIFSAVMSPAENPDFILYVTVQQPEHYSGIQL GQVALKSGTA+IADEKNGGYL G T+ IFS VSM PAENPDFILYVTVQQPEHYSGIQL	600
- Sbjct	541	GQVALKSGTAEIADEKNGGYLTGSTNNIFSVVSMHPAENPDFILYVTVQQPEHYSGIQL	600
Query	601	GEFANPILERASAMKDSLNLQTTAKALEQVSSQSPYPPMSVKDISPGDLAELRRNLVQP GEFANPILERASAMK+SLNLQTTAKALEQVSSQSPYPPMSVKDISPGDLAELRRNLVQP	660
Sbjct	601	GEFANPILERASAMKESLNLQTTAKALEQVSSQSPYPPMSVKDISPGDLAELRRNLVQP	660
Query	661	IVVGTGKIKNSSAEGKNLAPNQQVLILSDKAEEVPDMYWTKETAETLAKWLNIELEF IVVGTGKIKNSSAEGKNLAPNQQVLILSDKAEEVPDMYWTKETAET AKWLNIELEF	720
Sbjct	661	IVVGTGKIKNSSAEGKNLAPNQQVLILSDKAEEVPDMYWTKETAETFAKWLNIELEF	720
Query	721	QGSGSTVQKQDVRANTAIKDIKKITL LGD 750 +GSGSTVQKQDVRANTAIKDIKKITL LGD	750
Sbjct	721	EGSGSTVQKQDVRANTAIKDIKKITL LGD 750	

>dbj|BAD00920.1| penicillin-binding protein 2X [Streptococcus pneumoniae]
Length=750

Score = 1368 bits (3540), Expect = 0.0, Method: Composition-based stats.
Identities = 708/750 (94%), Positives = 731/750 (97%), Gaps = 0/750 (0%)

Query	1	MKWTKRVIKYATKNRKSPAENRRVGKSLSSL SVFVFAIFLVNFAVIIGTGTRFGTDLAK MKWTKRVIKYATKNRKSPAENRRVGKSLSSL SVFVFA+FLVNFAVIIGTGTRFGTDLAK	60
Sbjct	1	MKWTKRVIKYATKNRKSPAENRRVGKSLSSL SVFVFAFLVNFAVIIGTGTRFGTDLAK	60
Query	61	EAKKVHQTTRTVPAKRGTIYDRNGVPIAEDATS YNVYAVIDENYKSATGKILYVEKTQFN EAKKVHQTTRTVPAKRGTIYDRNGVPIAEDATS YNVYAVIDENYKSATGKILYVEKTQFN	120
Sbjct	61	EAKKVHQTTRTVPAKRGTIYDRNGVPIAEDATS YNVYAVIDENYKSATGKILYVEKTQFN	120
Query	121	KVAEVFH KYLDMEESYVREQLSQPNLKQVSFGAKGN GITYANMMSIKKELEAAEVKGIDF KVAEVFH KYLDMEESYVREQLSQPNLKQVSFG+KGN GITYANMMSIKKELE AEVKGIDF	180
Sbjct	121	KVAEVFH KYLDMEESYVREQLSQPNLKQVSFGSKGN GITYANMMSIKKELEAAEVKGIDF	180
Query	181	TTSPNRSPNGQFASSFIGLAQLHENE DGSKSLLGTSGMESSLNSILAGTDGIITYEKDR TTSPNRSPNGQFASSFIGLAQLHENE DGSKSLLGTSGMESSLNSILAGTDGIITYEKDR	240
Sbjct	181	TTSPNRSPNGQFASSFIGLAQLHENE DGSKSLLGTSGMESSLNSILAGTDGIITYEKDR	240
Query	241	LGNIVPGTEQVSQRTMDGKD VYTTIISPLQSF METQMDAFQE KVKGKYM TATL VS AKTGE LGNIVPGTEQVSQ+T+DGKD VYTTIIS LQS FMETQM+AFQE KVKGKYM TATL VS AKTGE	300
Sbjct	241	LGNIVPGTEQVSQQTVDGKD VYTTIISSTLQS FMETQMNAFQE KVKGKYM TATL VS AKTGE	300
Query	301	ILATTQRPTFDADTKEGITEDFWRDILYQSN YEPGSTMKVMLAAAIDNNTFPGEVFN ILATTQRPTFDADTKEG+T+DFWRDILYQSN YEPGSTMKVML AAAIDNNTFPGE FN	360
Sbjct	301	ILATTQRPTFDADTKEGLT KDFWRDILYQSN YEPGSTMKVMLAASIDNNTFPGEYFN	360
Query	361	SSELKIADATIR DWDVNEGLTGRMMTFSQGFAHSSNVGMTLLEQKMGDATWLDYLNRFK SSELKIAD TIRDWDVN+GLT GRMMTF QGFA SS NVGM+LLEQKMGDATWLDYLNRFK	420
Sbjct	361	SSELKIAD TIRDWDVN+GLT GRMMTF QGFA SS NVGM+LLEQKMGDATWLDYLNRFK	420
Query	421	FGVPTRFGLTDEYAGQLPADNIVNIAQSSFGQGISVTQTMQ IRAFTAIANDGVML EPKFI FGVPTRFGLTDEYAGQLPADNIVNIAQSSFGQGISVTQTM+RAFTAIANDGVML EPKFI	480
Sbjct	421	FGVPTRFGLTDEYAGQLPADNIVNIAQSSFGQGISVTQTMQ IRAFTAIANDGVML EPKFI	480
Query	481	SAIYDPNDQTARKSKQKEIVGNPVS KDAASLRT RTNMV LVG TD P VY GT MY NH STG KPTV T P SAIYD N+Q+ RKSQKEIVG PVS+DAASLRT NM+LVG TD P+Y GT MY NH TG K P+T P Sbjct	540
Sbjct	481	SAIYDTNNQSVRKSKQKEIVGKP VSE DAASLRT RTNMV ILV G TD PLY GT MY NH QTG K PII T P	540
Query	541	GQVALKSGTAQIADEKNGGYLVGLTDYIFSAVMSPAENPDFILYVTVQQPEHYSGIQL GQVALKSGTAQIADEKNGGYLVG T+YIFS V+M+PAENPDFILYVTVQQPEHYS QL	600
Sbjct	541	GQVALKSGTAQIADEKNGGYLVGST NYIFSVVTMNP AENPDFILYVTVQQPEHYSAAQL	600
Query	601	GEFANPILERASAMKDSLNLQTTAKALEQVSSQSPYPPMSVKDISPGDLAELRRNLVQP GEF+NPILERASAMKDSLNLQTTAKALEQVSSQSPYPPMSVKDISPGDLAELRRNLVQP	660
Sbjct	601	GEFSNPILERASAMKDSLNLQTTAKALEQVSSQSPYPPMSVKDISPGDLAELRRNLVQP	660
Query	661	IVVGTGKIKNSSAEGKNLAPNQQVLILSDKAEEVPDMYWTKETAETLAKWLNIELEF IVVGTGKIKNSSAEGKNLAPNQQVLILSDKAEEVPDMYWTK TAET AKWLNIELEF	720
Sbjct	661	IVVGTGKIKNSSAEGKNLAPNQQVLILSDKAEEVPDMYWTKATAETFAKWLNIELEF	720
Query	721	QGSGSTVQKQDVRANTAIKDIKKITL LGD 750 +GSGSTVQKQDVRANTAIKDIKKITL LGD	750
Sbjct	721	EGSGSTVQKQDVRANTAIKDIKKITL LGD 750	

>dbj|BAD00903.1| penicillin-binding protein 2X [Streptococcus pneumoniae]
Length=750

Score = 1367 bits (3538), Expect = 0.0, Method: Composition-based stats.
Identities = 705/750 (94%), Positives = 727/750 (96%), Gaps = 0/750 (0%)

Query 1 MKWTKRVIKYATKNRKSPAENRRVGKSLSSL SVFVFAIFLVNFAVIIGTGTRFGTDLAK 60

- Sbjct	1	MKWTKRVIKYATKNRKSPAENRRVGKSLSSLVFAIFLVNFAVIIGTGTRGTDLAK MKWTKRVIKYATKNRKSPAENRRVGKSLSSLVFAIFLVNFAVIIGTGTRGTDLAK	60
Query	61	EAKKVHQTRTVPAKRGTIYDRNGVPIAEDATSYNVYAVIDENYKSATGKILYVEKTQFN EAKKVHQTRTVPAKRGTIYDRNGVPIAEDATSYNVYAVIDENYKSATGKILYVEKTQFN	120
- Sbjct	61	EAKKVHQTRTVPAKRGTIYDRNGVPIAEDATSYNVYAVIDENYKSATGKILYVEKTQFN	120
Query	121	KVAEVFKYLDMEESYVREQLSQPNLKQVSFGAKGNITYANMMSIKKELEAAEVKGIDF KVAEVFKYLDMEESYVREQLSQPNLKQVSFGAKGNITYANMMSIKKELEAAEVKGIDF	180
Sbjct	121	KVAEVFKYLDMEESYVREQLSQPNLKQVSFGAKGNITYANMMSIKKELEAAEVKGIDF	180
Query	181	TTSPNRSPNGQFASSFIGLAQLHENEDGSKSLLGTSGMESSLNSILAGTDGIITYEKDR TTSPNRSPNGQFASSFIGLAQLHENEDGSKSLLGTSGMESSLNSILAGTDGIITYEKDR	240
Sbjct	181	TTSPNRSPNGQFASSFIGLAQLHENEDGSKSLLGTSGMESSLNSILAGTDGIITYEKDR	240
Query	241	LGNIVPGTEQVSQRTMDGKDVTYTTISPLQSFMETQMDAFQEVKVKGKYMATTLSAKTGE LGNIVPGTEQVSQRTMDGKDVTYTTISPLQSFMETQMDAFQEVKVKGKYMATTLSAKTGE	300
Sbjct	241	LGNIVPGTEQVSQRTMDGKDVTYTTISPLQSFMETQMDAFQEVKVKGKYMATTLSAKTGE	300
Query	301	ILATTQRPTFDADTKEGITEDFWRDILYQSNYEPGSTMVKVMLAAAIDNNTFPGEVFN ILATTQRPTFDADTKEGITEDFWRDILYQSNYEPGSTMVKVMLAAAIDNNTFPGEVFN	360
Sbjct	301	ILATTQRPTFDADTKEGITEDFWRDILYQSNYEPGSTMVKVMLAAAIDNNTFPGEVFN	360
Query	361	SSELKIADATIRDWDVNEGLTGRMMTFSQGFAHSSNVGMTLEQKMGDATWLDYLNRFK SSELKIADATIRDWDV+GLT G MMTFSQGFAHSSNVGM+LLEQKMGDATWLDYLNRFK	420
Sbjct	361	SSELKIADATIRDWDVNDGLTGGMMTFSQGFAHSSNVGMSLLEQKMGDATWLDYLNRFK	420
Query	421	FGVPTRFGLTDEYAGQLPADNIVNIAQSSFGQGISVTQTQMIRAFTAIANDGVMLEPKFI FGVPTRFGLTDEY GQLPADNIVNIA S+FGQGISVTQTQMIRAFTAIANDGVMLEPKFI	480
Sbjct	421	FGVPTRFGLTDEYTGQLPADNIVNIAMSAGQGISVTQTQMLRAFTAIANDGVMLEPKFI	480
Query	481	SAIYDPNDQTARKSQKEIVGNPVSKDAASLRTTNMVLVGTDPVYGTMYNHSTGKPTVTVP SAIYD N+Q+ RKS+KEIVG PVS+DAASLRTNM+LVGTD+YGTMYNH TGKP +TVP	540
Sbjct	481	SAIYDTNNQSVRKSKEIVGKPVSEDAASLRTTNMILVGTDPYGTMYNHHTGKPIITVP	540
Query	541	GQNVALKSGTAQIADEKNGGYLVGLTDYIFSAVSMSPAENPDFILYTVQQPEHYSGIQL GQNVA+KSGTAQIADEKNGGYLVG T+YIFS V+M+PAENPDFILYTVQQPEHYSGIQL	600
Sbjct	541	GQNVAVKSGTAQIADEKNGGYLVGSTNYIFSVVTMNPAAENPDFILYTVQQPEHYSGIQL	600
Query	601	GEFANPILERASAMKDSLNLQTTAKALEQVSQQSPYPMPSVKDISPGDLAELRRNLVQP GEFANPILERA AMKDSLNLQ+TAK L+QV+ QS Y MPS+KDISPGDLAE LRRN+VQP	660
Sbjct	601	GEFANPILERAVAMKDSLNLQSTAQLDQVTNQSAYAMPSIKDISPGDLAEALRRNIVQP	660
Query	661	IVVGTGTKIKNSSAEEGKNLAPNQQVLILSDKAEEVPDMYGTWTKETAETLAKWLNIELEF IVVGTGTKIK SS EEG NL PNQQVLILSDKAEEVPDMYGTWTK TAET AKWLNI+LEF	720
Sbjct	661	IVVGTGTKIKESSVEEGANLTPNQQVLILSDKAEEVPDMYGTWTKATAETFAKWLNI+LEF	720
Query	721	QGSGSTVQKQDVRANTAIKDIKKITLTG 750 +GSGSTVQKQDVRANTAIKDIKKITLTG	750
Sbjct	721	EGSGSTVQKQDVRANTAIKDIKKITLTG 750	750

>dbj|BAD00916.1| penicillin-binding protein 2X [Streptococcus pneumoniae]
Length=750

Score = 1365 bits (3534), Expect = 0.0, Method: Composition-based stats.
Identities = 706/750 (94%), Positives = 729/750 (97%), Gaps = 0/750 (0%)

Query	1	MKWTKRVIKYATKNRKSPAENRRVGKSLSSLVFAIFLVNFAVIIGTGTRGTDLAK MKWTKRVIKYATKNRKSPAENRRVGKSLSSLVFAIFLVNFAVIIGTGTRGTDLAK	60
Sbjct	1	MKWTKRVIKYATKNRKSPAENRRVGKSLSSLVFAIFLVNFAVIIGTGTRGTDLAK	60
Query	61	EAKKVHQTRTVPAKRGTIYDRNGVPIAEDATSYNVYAVIDENYKSATGKILYVEKTQFN EAKKVHQTRTVPAKRGTIYDRNGVPIAEDATSYNVYAVIDENYKSATGKILYVEKTQFN	120
Sbjct	61	EAKKVHQTRTVPAKRGTIYDRNGVPIAEDATSYNVYAVIDENYKSATGKILYVEKTQFN	120
Query	121	KVAEVFKYLDMEESYVREQLSQPNLKQVSFGAKGNITYANMMSIKKELEAAEVKGIDF KVAEVFKYLDMEESYVREQLSQPNLKQVSFGAKGNITYANMMSIKKELEAAEVKGIDF	180
Sbjct	121	KVAEVFKYLDMEESYVREQLSQPNLKQVSFGAKGNITYANMMSIKKELEAAEVKGIDF	180
Query	181	TTSPNRSPNGQFASSFIGLAQLHENEDGSKSLLGTSGMESSLNSILAGTDGIITYEKDR TTSPNRSPNGQFASSFIGLAQLHENEDGSKSLLGTSGMESSLNSILAGTDGIITYEKDR	240
Sbjct	181	TTSPNRSPNGQFASSFIGLAQLHENEDGSKSLLGTSGMESSLNSILAGTDGIITYEKDR	240
Query	241	LGNIVPGTEQVSQRTMDGKDVTYTTISPLQSFMETQMDAFQEVKVKGKYMATTLSAKTGE LGNIVPGTEQVSQRTMDGKDVTYTTISPLQSFMETQMDAFQEVKVKGKYMATTLSAKTGE	300
Sbjct	241	LGNIVPGTEQVSQRTMDGKDVTYTTISPLQSFMETQMDAFQEVKVKGKYMATTLSAKTGE	300
Query	301	ILATTQRPTFDADTKEGITEDFWRDILYQSNYEPGSTMVKVMLAAAIDNNTFPGEVFN ILATTQRPTFDADTKEG+T+DFWRDILYQSNYEPGSTMVKM LA+IDNNTFP GE FN	360
Sbjct	301	ILATTQRPTFDADTKEGLTDFWRDILYQSNYEPGSTMVKM TASSIDNNTFPSGEYFN	360
Query	361	SSELKIADATIRDWDVNEGLTGRMMTFSQGFAHSSNVGMTLEQKMGDATWLDYLNRFK SSELKIAD TIRDWDV+GLT GRMMTF QGFA SSNVGM+LLEQKMGD TWLDYLNRFK	420
Sbjct	361	SSELKIADVTIRDWDVNDGLTGGMMTFLQGFALSSNVGMSLLEQKMGDTWLDYLNRFK	420

NCBI Blast:PBP2X-R6

Query	421	FGVPTRFGLTDEYAGQLPADMINIVNIAQSSFGQGISVTQTQMIRAFTAIANDGVMLEPKFI FGVPTRFGLTDEYAGQLPADMINIVNIAQSSFGQGISVTQTQMIRAFTAIANDGVMLEPKFI	480
Sbjct	421	FGVPTRFGLTDEYAGQLPADMINIVNIAQSSFGQGISVTQTQMLRAFTAIANDGVMLEPKFI	480
Query	481	SAIYDPNDQTARKSQEIVGNPVSKDAASLRTNMVLVGTDPVYGTMYNHSTGKPTVTVP SAIYD N+Q+ RKSQEIVG PVS+DAASLRTNM+LVGTDP+YGTMYNH TGKP +TVP	540
Sbjct	481	SAIYDTNNQSVRKSQEIVGKPVSEDAASLRTNMILVGTDPYGTMYNHYTGKPIITVP	540
Query	541	GQNVALKSGTAQIADEKNGGYLVGLTDYIFSAVSMSPAENPDFILYVTVQQPEHSGIQL GQNVA+KSGTAQIADEKNGGYLVG T+YIFS V+M+PAENPDFILYVTVQQPEHSGIQL	600
Sbjct	541	GQNVAVKSGTAQIADEKNGGYLVGSTNYIFSVVTMNPENAEPDFILYVTVQQPEHSGIQL	600
Query	601	GEFANPILEASAMKDSLNLQTTAKALEQVSQSPYPMPSVKDISPGDLAELRRNLVQP GEFANPILEASAMK+SLNLQ+ AK L+QV+ +S Y MPS+KDISPGDLAELRRNLVQP	660
Sbjct	601	GEFANPILEASAMKESLNLQSPAQNLDQVTTESSYAMPSIKDISPGDLAELRRNLVQP	660
Query	661	IVVGTGKIKNSSAEGKNLAPNQQVLILSDKAEVVPDMYWTKETAETLAKWLNLIELEF IVVGTGKIKNSSAEGKNLAPNQQVLILSDK EEVVPDMYWTKETAETLAKWLNLIELEF	720
Sbjct	661	IVVGTGKIKNSSAEGKNLAPNQQVLILSDKVEEVVPDMYWTKETAETLAKWLNLIELEF	720
Query	721	QGSGSTVQKQDVRANTAIKDIKKITLTG 750 QGSGSTVQKQDVRANTAIKDIKKITLTG	750
Sbjct	721	QGSGSTVQKQDVRANTAIKDIKKITLTG 750	750

>gb|AAF17267.1|AF210757_1 penicillin-binding protein 2X [Streptococcus pneumoniae]
Length=750

Score = 1361 bits (3522), Expect = 0.0, Method: Composition-based stats.
Identities = 705/750 (94%), Positives = 726/750 (96%), Gaps = 0/750 (0%)

Query	1	MKWTKRVIRYATKNRKSPAENRRVGKSLSSLGVFAIFLNVFAVIIGTGTRGTDLAK MKWTKRVIRYATKNRKSPAENRRVGKSLSSLGVFA+FLVNFAVIIGTGTRGTDLAK	60
Sbjct	1	MKWTKRVIRYATKNRKSPAENRRVGKSLSSLGVFAVFLVNFAVIIGTGTRGTDLAK	60
Query	61	EAKKVHQTRRTVPAKRGTIYDRNGVPIAEDATSYNVYAVIDENYKSATGKILYVEKTQFN EAKKVHQTRR VPAKRGTIYDRNGVPIAEDATSYNVYAVIDENYKSATGKILYVEKTQFN	120
Sbjct	61	EAKKVHQTRTRIVPAKRGTIYDRNGVPIAEDATSYNVYAVIDENYKSATGKILYVEKTQFN	120
Query	121	KVAEVFKYLDMEESYVREQLSQPNLKQVSFGAKGNIGHTYANMMSIKKELEAAEVKGIDF KVAEVFKYLDMEESYVREQLSQPNLKQVSFGAKGNIGHTYANMMSIKKELE AEVKGIDF	180
Sbjct	121	KVAEVFKYLDMEESYVREQLSQPNLKQVSFGAKGNIGHTYANMMSIKKELEAAEVKGIDF	180
Query	181	TTSPNRSPNGQFASSFIGLAQLHENEDEDGSKSLLGTSGMESSLNSILAGTDGIITYEKDR TTSPNRSPNGQFASSFIGLAQLHENEDEDGSKSLLGTSGMESSLNSILAGTDGIITYEKDR	240
Sbjct	181	TTSPNRSPNGQFASSFIGLAQLHENEDEDGSKSLLGTSGMESSLNSILAGTDGIITYEKDR	240
Query	241	LGNIVPGTEQVSQRTMDGKDVDYTTIISPLQSFMETQMDAFQEKVKGKYMATLVSAKTGE LGNIVPGTEQVSQ+T+DGKDVDYTTIIS LQSFMETQMDAF EKVKGKYMATLVSAKTGE	300
Sbjct	241	LGNIVPGTEQVSQQTVDGKDVDYTTIISSTLQSFMETQMDAFLEKVKGKYMATLVSAKTGE	300
Query	301	ILATTQRPTFDADTKEGITEDFVWRDILYQSNYEPGSTMVKVMMLAAAIDNNTFPGEVFN ILATTQRPTF+ADTKEGITEDFVWRDILYQSNYEPGS MKVM LA+IDNNTFP GE FN	360
Sbjct	301	ILATTQRPTFNADTKEGITEDFVWRDILYQSNYEPGSAMVKVMTLASSIDNNTFPSGEYFN	360
Query	361	SSELKIADATIRDWDVNNEGLTGGRMMTFSQGFAHSSNVGMTLLEQKMGDATWLDYLNRFK SSE KIADAT RDWDVN+GLT G MMTF QGFAHSSNVGM+LLEQKMGDATWLDYL RFK	420
Sbjct	361	SSEFKIADATTRDWDVNNDGLTGGMMTFLQGFAHSSNVGMSLLEQKMGDATWLDYLRFK	420
Query	421	FGVPTRFGLTDEYAGQLPADMINIVNIAQSSFGQGISVTQTQMIRAFTAIANDGVMLEPKFI FGVPTRFGLTDEYAGQLPADMINIV+IAQSSFGQGISVTQTQMIRAFTAIANDGVMLEPKFI	480
Sbjct	421	FGVPTRFGLTDEYAGQLPADMINIVSIAQSSFGQGISVTQTQMLRAFTAIANDGVMLEPKFI	480
Query	481	SAIYDPNDQTARKSQEIVGNPVSKDAASLRTNMVLVGTDPVYGTMYNHSTGKPTVTVP SAIYD N+Q+ RKSQEIVG PVS+AAS TR +M+LVGTDP+YGTMYNH TGKP +TVP	540
Sbjct	481	SAIYDTNNQSVRKSQEIVGKPVSEDAASLRTNMILVGTDPYGTMYNHYTGKPIITVP	540
Query	541	GQNVALKSGTAQIADEKNGGYLVGLTDYIFSAVSMSPAENPDFILYVTVQQPEHSGIQL GQNVA+KSGTAQIADEKNGGYLVG T+YIFS V+M+PAENPDFILYVTVQQPEHSGIQL	600
Sbjct	541	GQNVAVKSGTAQIADEKNGGYLVGSTNYIFSVVTMNPENAEPDFILYVTVQQPEHSGIQL	600
Query	601	GEFANPILEASAMKDSLNLQTTAKALEQVSQSPYPMPSVKDISPGDLAELRRNLVQP GEFA PILERASAMKDSLNLQTTAKALEQVSQSPYPMPSVKDISPGDLAELRRNLVQP	660
Sbjct	601	GEFATPILEASAMKDSLNLQTTAKALEQVSQSPYPMPSVKDISPGDLAELRRNLVQP	660
Query	661	IVVGTGKIKNSSAEGKNLAPNQQVLILSDKAEVVPDMYWTKETAETLAKWLNLIELEF IVVGTGKIKNSSAEGKNLAPNQQVLILSDK EEVVPDMYWTKETAETLAKWLNLIELEF	720
Sbjct	661	IVVGTGKIKNSSAEGKNLAPNQQVLILSDKVEEVVPDMYWTKETAETLAKWLNLIELEF	720
Query	721	QGSGSTVQKQDVRANTAIKDIKKITLTG 750 QGSGSTVQKQDVRANTAIKDIKKITLTG	750
Sbjct	721	QGSGSTVQKQDVRANTAIKDIKKITLTG 750	750

>dbj|BAD00919.1| penicillin-binding protein 2X [Streptococcus pneumoniae]
Length=750

-	Score = 1357 bits (3511), Expect = 0.0, Method: Composition-based stats.
	Identities = 699/750 (93%), Positives = 726/750 (96%), Gaps = 0/750 (0%)
Query 1	MKWTKR VIRYAT KNRK SPAEN RRRVGKS LLS SVF VFA I FLVN FAVI I GTGTRFGTDLAK 60
-	MKWTK+ VIRYAT KNRK SPAEN RRRVGKS LLS SVF VFA+ FLVN FAVI I GTGTRFGTDLAK
Sbjct 1	MKWTKK VIRYAT KNRK SPAEN RRRVGKS LLS SVF VFA VFLVN FAVI I GTGTRFGTDLAK 60
Query 61	EAKKVH QTTRV PAKRGT I YDRNGVPIAEDATSYN VYAVIDENYKSATGKILYVEKTQFN 120
-	EAKKVH QTTRV PAKRGT I YDRNGVPIAEDATSYN VYAVIDENYKSATGKILYVEKTQFN
Sbjct 61	EAKKVH QTTRV PAKRGT I YDRNGVPIAEDATSYN VYAVIDENYKSATGKILYVEKTQFN 120
Query 121	KVAEV FH KYL DMEES YVREQLS QPNL KQVS FGAK GNGITYAN MMSIKKELEAAEVKGIDF 180
-	KVAEV FH KYL DMEES YVREQLS QPNL KQVS FGAK GNGITYAN MMSIKKELE AEVKGIDF
Sbjct 121	KVAEV FH KYL DMEES YVREQLS QPNL KQVS FGAK GNGITYAN MMSIKKELETAEVKGIDF 180
Query 181	TTSPNRSY PNGQF ASSFIGLAQ LHENEDGSKS LLLGTSGM ESSLNSI LAGTDGI ITYEKDR 240
-	TTSPNRSY PNGQF ASSFIGLAQ LHENEDGSKS LLLGTSGM ESSLNSI LAGDGI ITYEKDR
Sbjct 181	TTSPNRSY PNGQF ASSFIGLAQ LHENEDGSKS LLLGTSGM ESSLNSI LAGKDG I ITYEKDR 240
Query 241	LGNIVPGTE QVS QRTMDGKD VYT TISSPL QSF METQMDAFQEKVKGKYMTATL VS AKTGE 300
-	LGNIVPGTE QV Q+T+DGKD VYT TISS LQS FMETQM+AFQEKVKGKYMTATL VS AKTGE
Sbjct 241	LGNIVPGTE QV FQQTVDGKD VYT TISSL QS FMETQMNAFQEKVKGKYMTATL VS AKTGE 300
Query 301	I LAT TQRPTFDADTKEG I TEDF VWRD I LYQSN YEPG STM KVMM LAAA IDDN NTFP GGEV FN 360
-	I LAT TQRPTFDADTKEG+T+DFVWRD I LYQSN YEPG STM KVMM LAAA IDDN NTFP GGEV F+
Sbjct 301	I LAT TQRPTFDADTKEGLTKDFVWRD I LYQSN YEPG STM KVMT LAAA IDDN NTFP GGEV FD 360
Query 361	SSELKI ADATI RDWDV NEGLTGG RMM TFSQGF AHSS NVGM TLLEQ KMG D ATWLDY LNRFK 420
-	SSELKI AD TIRDWDV NEGLTGG RMM TFSQGF SSNV GM TLLEQ KMG D ATWLDY LNRFK
Sbjct 361	SSELKI ADVT I RDWDV NEGLTGG RMM TFSQGF VLSS NVGM TLLEQ KMG D ATWLDY LNRFK 420
Query 421	FGVPTRF GLTDEY AGQLPAD NIVNIAQ QSSFG QGI S VTQ TQMI R AFTAI ANDGV MLEPKFI 480
-	FGVPTRF GLTDEY AGQLPAD NIVNIAQ QSSFG QGI S VTQ TQMI R AFTAI ANDGV MLEPKFI
Sbjct 421	FGVPTRF GLTDEY AGQLPAD NIVNIAQ QSSFG QGI S VTQ TQMI R AFTAI ANDGV MLEPKFI 480
Query 481	SAI YDPNDQ TARKS QKE I VGNP VS KDA ASL TRTNMVL VGT DPVY GTM NHSTG KPTV TVP 540
-	SA + YDPNDQ+ RKS QKE I VGNP VS K+AAS+TR MV+VGT DPVY GTM NHSTG KPTV TVP
Sbjct 481	SAL YDPNDQ S VRK S QKE I VGNP VS KEA ASV TRD YMVM VG TD PVY GTM NHSTG KPTV TVP 540
Query 541	GQNVAL KSG TAQ IADE KNGGY LVGL TDY I FSAV S MPAEN PDF I LYVTV QQP EHY SG IQL 600
-	GQNVAL KSG TAQ IADE KNGGY LVGL T+Y I FSAV S M+PAEN PDF I LYVTV QQP EHY SG IQL
Sbjct 541	GQNVAL KSG TAQ IADE KNGGY LVGL NY I FSAV S MNP AEN PDF I LYVTV QQP EHY SG IQL 600
Query 601	GEFANP I LERASAM KDSL NLQTTAKALEQV SQSPY PMPSV KDI SPGD LAEL RRNL VQP 660
-	GEFANP I LERA AMKDSL NLQ+TAKAL+Q+S Q+ Y MPS+KDI SPGD LAEL RRN+VQP
Sbjct 601	GEFANP I LERA VAM KDSL NLQSTA KALDQI SSQTSY AMPSIKD I SPGD LAEL RRNI VQP 660
Query 661	I VVGTG TKI KNSSAEEG KNLAPN QQVL L I LSDK KAEE VPDM YGW T KETA ET LAKWLNIELEF 720
-	I VVGTG TKI K+S EEG NLAPN QQVL+LSDK EE+PD MY GW KETA ET AKWL+IELEF
Sbjct 661	I VVGTG TKI KETS VEE GTN LAPN QQV L LSDK VEE I PD MY GW KETA ET FAKWLDIELEF 720
Query 721	QGSGST VQ KQD VR RANTAI KDI KIT LTLGD 750
-	+GSGS VQ KQD VR NTAIK+IKKI LTLGD
Sbjct 721	EGSGSV VQ KQD VR NT A I KNI KIK LTLGD 750

>gb|AAF17264.1|AF210754_1 penicillin-binding protein 2X [Streptococcus pneumoniae]
Length=750

Score = 1349 bits (3492), Expect = 0.0, Method: Composition-based stats.	
Identities = 696/750 (92%), Positives = 725/750 (96%), Gaps = 0/750 (0%)	
Query 1	MKWTKR VIRYAT KNRK SPAEN RRRVGKS LLS SVF VFA I FLVN FAVI I GTGTRFGTDLAK 60
-	MKWTK+ VIRYAT KNRK SPAEN RRRVGKS LLS SVF VFA+ FLVN FAVI I GTGTRFGTDLAK
Sbjct 1	MKWTKK VIRYAT KNRK SPAEN RRRVGKS LLS SVF VFA VFLVN FAVI I GTGTRFGTDLAK 60
Query 61	EAKKVH QTTRV PAKRGT I YDRNGVPIAEDATSYN VYAVIDENYKSATGKILYVEKTQFN 120
-	EAKKVH QTTRV PAKRGT I YDRNGVPIAEDATSYN VYAVIDENYKSATGKILYVEKTQFN
Sbjct 61	EAKKVH QTTRV PAKRGT I YDRNGVPIAEDATSYN VYAVIDENYKSATGKILYVEKTQFN 120
Query 121	KVAEV FH KYL DMEES YVREQLS QPNL KQVS FGAK GNGITYAN MMSIKKELEAAEVKGIDF 180
-	KVAEV FH KYL DMEES YVREQLS QPNL KQVS FG+KNGNITYAN MM+IKKELE AEVKGIDF
Sbjct 121	KVAEV FH KYL DMEES YVREQLS QPNL KQVS FGSK GNGITYAN MMAIKKELETAEVKGIDF 180
Query 181	TTSPNRSY PNGQF ASSFIGLAQ LHENEDGSKS LLLGTSGM ESSLNSI LAGTDGI ITYEKDR 240
-	TTSPNRSY PNGQF ASSFIGLAQ LHENEDGSKS LLLGTSGM ESSLNSI LAGDGI ITYEKDR
Sbjct 181	TTSPNRSY PNGQF ASSFIGLAQ LHENEDGSKS LLLGTSGM ESSLNSI LAGKDG I ITYEKDR 240
Query 241	LGNIVPGTE QVS QRTMDGKD VYT TISSPL QSF METQMDAFQEKVKGKYMTATL VS AKTGE 300
-	LGNIVPGTE QV Q+T+DGKD VYT TISS LQS FMETQM+AFQEKVKGKYMTATL VS AKTGE
Sbjct 241	LGNIVPGTE QV FQQTVDGKD VYT TISSL QS FMETQMNAFQEKVKGKYMTATL VS AKTGE 300
Query 301	I LAT TQRPTFDADTKEG I TEDF VWRD I LYQSN YEPG STM KVMM LAAA IDDN NTFP GGEV FN 360
-	I LAT TQRPTFDADTKEG+T+DFVWRD I LYQSN YEPG STM KVMM LAAA IDDN NTFP GGEV FN
Sbjct 301	I LAT TQRPTFDADTKEGLTKDFVWRD I LYQSN YEPG STM KVMT LAAA IDDN NTFP GGEV FN 360

-Query	361	SSELKIADATIRDWDVNEGLTGGGRMMTFSQGFAHSSNVGMTLLEQKMGDATWLDYLNRFK	420
Sbjct	361	SSELKIADATIRDWDVNEGLTGGGRMMTFSQGFAHSSNVGMTLLEQKMGDATWLDYLNRFK	420
-Query	421	FGVPTRFGLTDEYAGQLPADMINVIAQSSFGQGISVTQTQMIRAFTAIANDGVMLEPKFI	480
Sbjct	421	FGVPTRFGLTDEYAGQLPADMINVIAQSSFGQGISVTQTQMIRAFTAIANDGVMLEPKFI	480
Query	481	SAIYDPNDQTARKSQKEIVGNPVSCKDAASLTTRTNMVLVGTDPVYGTMYNHSTGKPTVTVP	540
Sbjct	481	+A+YDPN+Q+ RKSQKEIVGNPVSCKDAAS TRT+MVLVGTDP YGTMYNHSTGK TV VP TALYDPNNQSVRKSQKEIVGNPVSCKDAASQTRTHMVLVGTDPYGTMYNHSTGKATVNVP	540
Query	541	GQVALKSGTAQIADEKNGGYLVGLTDYIFSAVSMSPAENPDFILYVTVQQPEHYSGIQL	600
Sbjct	541	GQVALKSGTAQIADEKNGGYLVG T++IFS V+M+PAENPDFILYVTVQQPEHYSGIQL	600
Query	601	GEFANPILESAMKDSLNLQTTAKALEQVSQQSPYPMPSVKDISPGDLAEELRRNLVQP	660
Sbjct	601	GEFANPILEARA MKDSLNLQ+TAK L+QV+ QS Y MPS+KDISPGDLAE LRRN+VQP GEFANPILEAVAMKDSLNLQSTAKTLQDVTNQSAYAMPSIKDISPGDLAEALRRNIVQP	660
Query	661	IVVGTGTKIKNSSAEGKNLAPNQQVLILSDKAEEVPDMYWTKETAETLAKWLNLIEF	720
Sbjct	661	IVVGTGTKIK SS EEG NLAPNQQVL+LSDKAEEVPDMYWTK TAE +KWLNLIEL F IVVGTGTKIKESSVEEGSNLAPNQQVLLSDKAEEVPDMYWTKATAEAFSKWLNLIELVF	720
Query	721	QGSGSTVQKQDVRANTAIKDIKKITLTLGD 750	
Sbjct	721	+GSGSTVQKQDVRANTAIKDIKKITLTLGD EGSGSTVQKQDVRANTAIKDIKKITLTLGD 750	

>dbj|BAD00929.1| penicillin-binding protein 2X [Streptococcus pneumoniae]
Length=750

Score = 1348 bits (3489), Expect = 0.0, Method: Composition-based stats.
Identities = 695/750 (92%), Positives = 724/750 (96%), Gaps = 0/750 (0%)

Query	1	MKWTKR VIRYATK NRK SPA ENRR RVG KSL SLL SVF VFA I FL VN FA VI I GT GTR FG TD LAK	60
Sbjct	1	MKWTKK VIRYATK NRK SPA ENRR RVG KSL SLL SVF VFA +FL VN FA VI I GT GTR FG TD LAK	60
Query	61	EAKKVHQ TTR TV PAK RGT I YDR NGVPI AED AT SYN VY AVI DEN YK SAT GK I LY VE KT QFN	120
Sbjct	61	EAKKVHQ TTR TV PAK RGT I YDR NGVPI AED AT SYN VY AVI DEN YK SAT GK I LY VE KT QFN	120
Query	121	KVAEV FH KY LD MEES YV RE QL SQ PN LK QV SF GA KGN GITY AN MMS IK KE LEAA EV KG ID F	180
Sbjct	121	KVAEV FH KY LD MEES YV RE QL SQ PN LK QV SF GA KGN GITY AN MMS IK KE LEAA EV KG ID F	180
Query	181	TTSPNR SY PNG QF ASS FIG LAQ L HEN ED GS K SLL GT SG MESS L N S I AG D G I I T Y E K D R	240
Sbjct	181	TTSPNR SY PNG QF ASS FIG LAQ L HEN ED GS K SLL GT SG MESS L N S I AG D G I I T Y E K D R	240
Query	241	LGNIV PGTE QV S QRT MDG KDV YTT I S S P L Q S F M E T Q M D A F Q E K V K G K Y M T A T L V S A K T G E	300
Sbjct	241	LGNIV PGTE QV S Q +T+DG KDV YTT I S S P L Q S F M E T Q M A F Q E K V K G K Y M T A T L V S A K T G E	300
Query	301	I LATT QR PT FD ADT KEG I T EDF W R D I L Y Q S N Y E P G S T M K V M M L A A I D N N T F P G G E V F N	360
Sbjct	301	I LATT QR PT FD ADT KEG I T +DF W R D I L Y Q S N Y E P G S T M K V M L A A I D N N T F P G G E V F N	360
Query	361	SSELKIADATIRDWDVNEGLTGGGRMMTFSQGFAHSSNVGMTLLEQKMGDATWLDYLNRFK	420
Sbjct	361	SSELKIAD TIRDWDVN+GLT GRMMTF QGFA SSVGM+LLEQKMGDATWLDYLNRFK	420
Query	421	FGVPTRFGLTDEYAGQLPADMINVIAQSSFGQGISVTQTQMIRAFTAIANDGVMLEPKFI	480
Sbjct	421	FGVPTRFGLTDEYAGQLPADMINVIAQSSFGQGISVTQTQMIRAFTAIANDGVMLEPKFI	480
Query	481	SAIYDPNDQTARKSQKEIVGNPVSCKDAASLTTRTNMVLVGTDPVYGTMYNHSTGKPTVTVP	540
Sbjct	481	SAIYDPNDQTARKSQKEIVGNPVSCKDAASLTTRTNMVLVGTDPVYGTMYNH TGKP +TV P SAIYDPNDQTARKSQKEIVGNPVSCKDAASLTTRTNMVLVGTDPVYGTMYNH QTGKPI ITVP	540
Query	541	GQVALKSGTAQIADEKNGGYLVGLTDYIFSAVSMSPAENPDFILYVTVQQPEHYSGIQL	600
Sbjct	541	GQVA+KSGTAQIADEKNGGYLVG T+YIFS V+M+PAENPDFILYVTVQQPEHYS +QL GQNVA V KSGTAQIADEKNGGYLVGST NY I FSV VT MN PAEN PDFILYVTVQQPEHYS A V Q L	600
Query	601	GEFANPILESAMKDSLNLQTTAKALEQVSQQSPYPMPSVKDISPGDLAEELRRNLVQP	660
Sbjct	601	GEF+NPILESAMK+SLNLQ+ AK L+QV+ +S Y MPS+KDISPGDLAE LRRN+VQP GEFSNPILERASAMKESLNLQSPAKNLDQVTTESSYAMPSIKDISPGDLAEALRRNIVQP	660
Query	661	IVVGTGTKIKNSSAEGKNLAPNQQVLILSDKAEEVPDMYWTKETAETLAKWLNLIEF	720
Sbjct	661	IVVGTGTKIK +S EEG KNLAPNQQVL+LSDK EE+PD MYWTK TAE +KWLNLIEL F IVVGTGTKIKETSVEEGKNLAPNQQVLLSDKVEEIPDMYWTKATAEAFSKWLNLIELVF	720
Query	721	QGSGSTVQKQDVRANTAIKDIKKITLTLGD 750	
Sbjct	721	+GSGSTVQKQDVRANTAIKDIKKITLTLGD	

Sbjct 721 ESGGSTVQKQDVRANTAIKDIKKITLTLGD 750

>dbj|BAD00909.1| penicillin-binding protein 2X [Streptococcus pneumoniae]
Length=750

Score = 1345 bits (3481), Expect = 0.0, Method: Composition-based stats.
Identities = 693/750 (92%), Positives = 720/750 (96%), Gaps = 0/750 (0%)

Query 1	MKWTKR VIRYAT KNRK SPAEN RRRVGK SLSLLS VFVAI FFLVNFAVI IGTGTRGTD LAK MKWTKR VIRYAT KNRK SPAEN RRRVGK SLSLLS VFVA+ FFLVNFAVI IGTGTRGTD LAK	60
Sbjct 1	MKWTKR VIRYAT KNRK SPAEN RRRVGK SLSLLS VFVAF FLVNFAVI IGTGTRGTD LAK	60
Query 61	EAKKVHQ TTRVPAKRG TIYDRNGVPIAEDATSYN VYAVIDEN YKSATGKILYVEKTQFN EAKKVHQ TTRVPAKRG TIYDRNGVPIAED TSYN VYAVIDEN YKSATGKILYVEKTQFN	120
Sbjct 61	EAKKVHQ TTRVPAKRG TIYDRNGVPIAEDETSYN VYAVIDEN YKSATGKILYVEKTQFN	120
Query 121	KVAEV FH KYLDMEES YVREQL SQPNLK QVSFGAKGN GITYANMMSIKKELEAAEVKGIDF KVAEV FH KYLDMEES YVREQL SQPNLK QVSFGAKGN GITYANMMSIKKELEAEVKGIDF	180
Sbjct 121	KVAEV FH KYLDMEES YVREQL SQPNLK QVSFGAKGN GITYANMMSIKKELEAEVKGIDF	180
Query 181	TTSPNRSYPNGQFASSFIGLAQLHENE DGSKSLLGTSGMESSLNSILAGTDGIITYEKDR TTSPNRSYPNGQFASSFIGLAQLHENE DGSKSLLGTSGMESSLNSILAGTDGIITYEKDR	240
Sbjct 181	TTSPNRSYPNGQFASSFIGLAQLHENE DGSKSLLGTSGMESSLNSILAGTDGIITYEKDR	240
Query 241	LGNIVPGTEQVSQRTMDGKD VYT TISSPLQS FMETQMDAFQE KVKGK YM TATL VS A KTG LGNIVPGTEQVSQ +T+ DGKD VYT TISSPLQS FMETQMDAFQE KVKGK YM TATL VS A KTG	300
Sbjct 241	LGNIVPGTEQVSQQTVDGKD VYT TISSPLQS FMETQMDAFQE KVKGK YM TATL VS A KTG	300
Query 301	I LATTQRPTFDADTKEG I TDFW RDILYQSN YEPG STMKV MM LAAAIDNNTFPGGEVFN I LATTQRPTFDADTKEG +T+ DFVW RDILYQSN YEPG S MKVM LA+ IDNNTFPGGE FN	360
Sbjct 301	I LATTQRPTFDADTKEGLT KDFV WRDILYQSN YEPG SAMKV MTLASSIDNNTFPGGEYFN	360
Query 361	SSELKIADATIR DW DVNE GLTGG RMM TFSQG FAHSS NVGM TLLEQ KM GDATWL DYL NR FK SSELKIADAT RD DW DVNE GLT G MMTFSQG FAHSS NVGM +LLEQ KM GDATWL DYL NR FK	420
Sbjct 361	SSELKIADVT RD DW DVNE GLT VGG MMTFSQG FAHSS NVGM SLLEQ KM GDATWL DYL NR FK	420
Query 421	FGVP TRFGLTDEYAG QLPAD NIVNIAQSSFGQGISV TQTM IRFTA IANDGVML EPKFI FGVP TRFGLTDEYAG QLPAD NIVNIAQSSFGQGISV TQTM IRFTA IANDGVML EPKFI	480
Sbjct 421	FGVP TRFGLTDEYAG QLPAD NIVNIAQSSFGQGISV TQTM IRFTA IANDGVML EPKFI	480
Query 481	SAIYDPNDQTARKS QKEIV GNPV SKDAAS LTR TNMVL VGT DPV YGT MYNH STG KPTV T VP +A+YDPNDQT RKS QKEIV GNPV SKDAAS TRT +MVL VGT DP+Y GT MYNH TGKP +T VP	540
Sbjct 481	TAL YDPNDQT VRKS QKEIV GNPV SKDAAS QTR THM VL VGT DP YGT MYNH QTG KPI IT VP	540
Query 541	GQNVAL KSGTAQIA DEKNGGYLV GLTDY IFS AVS MSPA ENP DFI LYV TVQ QPEH YSGIQL GQNVA +KSGTAQIA DEKNGGYLV G T+YIFS V +M+ PAENP DFI LYV TVQ QPEH YSGIQL	600
Sbjct 541	GQNVAVKSGTAQIA DEKNGGYLV GST NYIF SVV TMNPA ENP DFI LYV TVQ QPEH YSGIQL	600
Query 601	GEFANP ILERASAM KDSL NLQTTAKALEQV SQQSPY PMPS VKD I SPGD LAE ELRRN LVQP GEFANP ILERA AMKDSL NLQ +TAK L +QV +QS Y MPS +KDI SPGD LAE LRRN +VQP	660
Sbjct 601	GEFANP ILERA VAM KDSL NLQSTAK TL DQV TNQ SAYAMPSI KDI SPGD LAE ALRRN IVQP	660
Query 661	IVVGTG TKIKN SSAEEG KNLAPN QQVL LILSDKAEE VPDM YGWT KETAETL AKWL NI ELE F IVVGTG TKIK SS EEG NLAPN QQVL +LSDKAEE VPDM YGWT K TAE +KWL NI E+ F	720
Sbjct 661	IVVGTG TKIK ESSVEEGTN LAPN QQV LLLSDKAEE VPDM YGWT KATAE AF SKWL NI EIV F	720
Query 721	QGGGSTVQKQDVRANTAIKDIKKITLTLGD 750 +GSGGSTVQKQDVRANTAIKDIKKITLTLGD	750
Sbjct 721	EGSGGSTVQKQDVRANTAIKDIKKITLTLGD 750	750

>dbj|BAD00907.1| penicillin-binding protein 2X [Streptococcus pneumoniae]
Length=750

Score = 1344 bits (3478), Expect = 0.0, Method: Composition-based stats.
Identities = 691/750 (92%), Positives = 721/750 (96%), Gaps = 0/750 (0%)

Query 1	MKWTKR VIRYAT KNRK SPAEN RRRVGK SLSLLS VFVAI FFLVNFAVI IGTGTRGTD LAK MKWTKR VIRYAT KNRK SPAEN RRRVGK SLSLLS VFVAI FFLVNFAVI IGTGTRGTD LAK	60
Sbjct 1	MKWTKR VIRYAT KNRK SPAEN RRRVGK SLSLLS VFVAI FFLVNFAVI IGTGTRGTD LAK	60
Query 61	EAKKVHQ TTRVPAKRG TIYDRNGVPIAEDATSYN VYAVIDEN YKSATGKILYVEKTQFN EAKKVHQ TTRVPAKRG TIYDRNGVPIAEDATSYN VYAVIDEN YKSATGKILYVEKTQFN	120
Sbjct 61	EAKKVHQ TTRVPAKRG TIYDRNGVPIAEDATSYN VYAVIDEN YKSATGKILYVEKTQFN	120
Query 121	KVAEV FH KYLDMEES YVREQL SQPNLK QVSFGAKGN GITYANMMSIKKELEAAEVKGIDF KVAEV FH KYLDMEES YVREQL SQPNLK QVSFGAKGN GITYANMMSIKKELEAAEVKGIDF	180
Sbjct 121	KVAEV FH KYLDMEES YVREQL SQPNLK QVSFGAKGN GITYANMMSIKKELEAAEVKGIDF	180
Query 181	TTSPNRSYPNGQFASSFIGLAQLHENE DGSKSLLGTSGMESSLNSILAGTDGIITYEKDR TTSPNRSYPNGQFASSFIGLAQLHENE DGSKSLLGTSGMESSLNSILAGTDGIITYEKDR	240
Sbjct 181	TTSPNRSYPNGQFASSFIGLAQLHENE DGSKSLLGTSGMESSLNSILAGTDGIITYEKDR	240
Query 241	LGNIVPGTEQVSQRTMDGKD VYT TISSPLQS FMETQMDAFQE KVKGK YM TATL VS A KTG LGNIVPGTEQVSQRTMDGKD VYT TISSPLQS FMETQMDAFQE KVKGK YM TATL VS A KTG	300

NCBI Blast:PBP2X-R6

Sbjct	241	LGNIVPGTEQVSQRTMDGKDVTISSLQSFMETQMDAFQEKVKGKYMATLVSAKTGE	300
Query	301	I LAT TQRPTFDADTKEGIT EDFVWRDILYQSNYEPGSTMVKVMM LAAAIDNNTFPGEVFN	360
Sbjct	301	I LAT TQRPTFDADTKEGIT EDFVWRDILYQSNYEPGSTMVKVMM LAAAIDNNTFPGEVFN	360
Query	361	SSELKIADATIRDWDVNEGLTGGRMMTFSQGFAHSSNVGMTLLEQKMGDATWLDYLNRFK	420
Sbjct	361	SSELKIADATIRDWDVNEGLTGGRMMTFSQGFAHSSNVGMTLLEQKMGDATWLDYLNRFK	420
Query	421	FGVPTRFGLTDEYAGQLP PADNIVNIAQSSFGQG I SVTQTQMI R AFTAI ANDGVML EPKFI	480
Sbjct	421	FGVPTRFGLTDEYAGQLP PADNIVNIAQSSFGQG I SVTQTQMI R AFTAI ANDGVML EPKFI	480
Query	481	SAI YDPNDQTARKS QKE I VGNPVSKDAASLRTTNMVLVGTDPVYGT MHN STGKPTVTPV	540
Sbjct	481	SAI YD N+Q+ RKS QKE I VG PVS+DAASLRTTNM+LVGTDP+YGT MHN TGKP +TVP	540
Query	541	GQNVALKSGTAQIADEKNGGYLVGLTDYI FSAVSMSPAENPDFI LYVTVQQPEHYSGIQL	600
Sbjct	541	GQNVALKSGTAQIADEKNGGYLVGLTDYI FSAVSMSPAENPDFI LYVTVQQPEHYSGIQL	600
Query	601	GEFANPILERASAMKDSLNLQTTAKALEQVSPQSPYPMPSVKDISPGDLAEELRRNLVQP	660
Sbjct	601	GEFANPILERASAMK+SLNLQ+ AK L+QV+ +S Y MPS+KDISPGDLAE LRRN+VQP	660
Query	661	IVVGTGTKIKNSSAEEGKNLAPNQQVLILSDKAEEVPDMYGWT KETAETLAKWL NIELEF	720
Sbjct	661	IVVGTGTKIK +S EEGKNLAPNQQVL+LSDK EE+PD MYGW KETAET AKWL+IELEF	720
Query	721	QGSGSTVQKQDVR RANTAI KDIKKITLT LGD 750	
Sbjct	721	+GSGS VQKQDVR NTAIK+IKKI LT LGD 750	

> pdb|1QME|A S Chain A, Penicillin-Binding Protein 2x (Pbp-2x)

pdb|1QMF|A S Chain A, Penicillin-Binding Protein 2x (Pbp-2x) Acyl-Enzyme Complex
Length=702

		Score = 1344 bits (3478), Expect = 0.0, Method: Composition-based stats.
		Identities = 702/702 (100%), Positives = 702/702 (100%), Gaps = 0/702 (0%)
Query	49	GTGTRFGTDLAKEAKKVHQTTRTVPAKRG TI YDRNGVPIAEDATS YN VYAVI DENYKSAT
Sbjct	1	GTGTRFGTDLAKEAKKVHQTTRTVPAKRG TI YDRNGVPIAEDATS YN VYAVI DENYKSAT
Query	109	GKILYVEKTQFNKVAEVFHKYLDMEESYVREQLSQPNLKQVSGFAKGN GITYANMMSI KK
Sbjct	61	GKILYVEKTQFNKVAEVFHKYLDMEESYVREQLSQPNLKQVSGFAKGN GITYANMMSI KK
Query	169	ELEAAEVKGIDFTTSPNRSYPNGQFASSFIGLAQLHENEDGSKSLLGTSGMESSLNSILA
Sbjct	121	ELEAAEVKGIDFTTSPNRSYPNGQFASSFIGLAQLHENEDGSKSLLGTSGMESSLNSILA
Query	229	GTDGI ITYEKDR LGNIVPGTEQVSQRTMDGKDVTISSLQSFMETQMDAFQE KVKGKY
Sbjct	181	GTDGI ITYEKDR LGNIVPGTEQVSQRTMDGKDVTISSLQSFMETQMDAFQE KVKGKY
Query	289	MTATLVSAKTGEI LAT TQRPTFDADTKEGIT EDFVWRDILYQSNYEPGSTMVKVMM LAAA
Sbjct	241	MTATLVSAKTGEI LAT TQRPTFDADTKEGIT EDFVWRDILYQSNYEPGSTMVKVMM LAAA
Query	349	DNNTFPGGEVFNSSELKIADATIRDW DVNEGLTGGRMMTFSQGFAHSSNVGMTLLEQKMG
Sbjct	301	DNNTFPGGEVFNSSELKIADATIRDW DVNEGLTGGRMMTFSQGFAHSSNVGMTLLEQKMG
Query	409	DATWLDYLNRFKFGVPTRFGLTDEYAGQLP ADNIVNIAQSSFGQG I SVTQTQMI R AFTAI
Sbjct	361	DATWLDYLNRFKFGVPTRFGLTDEYAGQLP ADNIVNIAQSSFGQG I SVTQTQMI R AFTAI
Query	469	ANDGVMLEPKFISAIYDPNDQTARKS QKE I VGNPVSKDAASLRTTNMVLVGTDPVYGTMY
Sbjct	421	ANDGVMLEPKFISAIYDPNDQTARKS QKE I VGNPVSKDAASLRTTNMVLVGTDPVYGTMY
Query	529	NHSTGKPTVTPGQNVALKSGTAQIADEKNGGYLVGLTDYI FSAVSMSPAENPDFI LYVT
Sbjct	481	NHSTGKPTVTPGQNVALKSGTAQIADEKNGGYLVGLTDYI FSAVSMSPAENPDFI LYVT
Query	589	VQQPEHYSIGIQLGEFANPILERASAMKDSLNLQTTAKALEQVSOQS PYPMP SVKD ISPGD
Sbjct	541	VQQPEHYSIGIQLGEFANPILERASAMKDSLNLQTTAKALEQVSOQS PYPMP SVKD ISPGD
Query	649	LAEELRRNLVQPIVVGTGTKIKNSSAEEGKNLAPNQQVLILSDKAEEVPDMYGWT KETA E
		LAEELRRNLVQPIVVGTGTKIKNSSAEEGKNLAPNQQVLILSDKAEEVPDMYGWT KETA E

Sbjct	601	LAEELRRNLVQPIVVGTGKIKNSSAEEGKNLAPNQQVLILSDKAEEVPDMYGWTKETAE	660
Query	709	TLAKWLNLIELEFQGSGSTVQKQDVRANTAIKDIKKITLTLGD	750
Sbjct	661	TLAKWLNLIELEFQGSGSTVQKQDVRANTAIKDIKKITLTLGD	702

> pdb|1PYY|A S Chain A, Double Mutant Pbp2x T338aM339F FROM STREPTOCOCCUS Pneumoniae Strain R6 At 2.4 A Resolution Length=702

Score = 1341 bits (3471), Expect = 0.0, Method: Composition-based stats.
Identities = 700/702 (99%), Positives = 700/702 (99%), Gaps = 0/702 (0%)

Query	49	GTGTRFGTDLAKEAKKVHQTTTRVPAKRGTIYDRNGVPIAEDATSYNVYAVIDENYKSAT	108
Sbjct	1	GTGTRFGTDLAKEAKKVHQTTTRVPAKRGTIYDRNGVPIAEDATSYNVYAVIDENYKSAT	60
Query	109	GKILYVEKTQFNKVAEVFKYLDMEESYVREQLSQPNLKQVSFGAKGNIGITYANMMSIKK	168
Sbjct	61	GKILYVEKTQFNKVAEVFKYLDMEESYVREQLSQPNLKQVSFGAKGNIGITYANMMSIKK	120
Query	169	ELEAAEVKGIDFTTSPNRSPNGQFASSFIGLAQLHENEDGSKSLLGTSGMESSLNSILA	228
Sbjct	121	ELEAAEVKGIDFTTSPNRSPNGQFASSFIGLAQLHENEDGSKSLLGTSGMESSLNSILA	180
Query	229	GTDGIITYEKDRLGNIVPGTEQVSQRTMDGKDVTIISPLQSFMETQMDAFQEKVKGKY	288
Sbjct	181	GTDGIITYEKDRLGNIVPGTEQVSQRTMDGKDVTIISPLQSFMETQMDAFQEKVKGKY	240
Query	289	MTATLVSAKTGEILATTQRPTFDADTKEGITEDFVWRDILYQSNYEPGSTMVKVMMIAAAI	348
Sbjct	241	MTATLVSAKTGEILATTQRPTFDADTKEGITEDFVWRDILYQSNYEPGSAFKVMMIAAAI	300
Query	349	DNNTFPGGEVFNSSELKIADATIRDWDVNNEGLTGGRMMTFSQGFAHSSNVGMTLLEQKMG	408
Sbjct	301	DNNTFPGGEVFNSSELKIADATIRDWDVNNEGLTGGRMMTFSQGFAHSSNVGMTLLEQKMG	360
Query	409	DATWLDYLNRFKFGVPTRFGLTDEYAGQLPADNIVNIAQSSFGQGIVSQTQMIRAFTAI	468
Sbjct	361	DATWLDYLNRFKFGVPTRFGLTDEYAGQLPADNIVNIAQSSFGQGIVSQTQMIRAFTAI	420
Query	469	ANDGVMLEPKFISAIYDPNDQTARKSQKEIVGNPVSKDAASLRTNMVLVGTDPVYGTMY	528
Sbjct	421	ANDGVMLEPKFISAIYDPNDQTARKSQKEIVGNPVSKDAASLRTNMVLVGTDPVYGTMY	480
Query	529	NHSTGKPTVTVPQNVALKSGTAQIADEKNGGYLVGLTDYIFSAVSMSPAENPDFILYVT	588
Sbjct	481	NHSTGKPTVTVPQNVALKSGTAQIADEKNGGYLVGLTDYIFSAVSMSPAENPDFILYVT	540
Query	589	VQQPEHSGIQLGEFANPILERASAMKDSLNLQTTAKALEQVSQQSPYPMPSPVKDISPGD	648
Sbjct	541	VQQPEHSGIQLGEFANPILERASAMKDSLNLQTTAKALEQVSQQSPYPMPSPVKDISPGD	600
Query	649	LAEELRRNLVQPIVVGTGKIKNSSAEEGKNLAPNQQVLILSDKAEEVPDMYGWTKETAE	708
Sbjct	601	LAEELRRNLVQPIVVGTGKIKNSSAEEGKNLAPNQQVLILSDKAEEVPDMYGWTKETAE	660
Query	709	TLAKWLNLIELEFQGSGSTVQKQDVRANTAIKDIKKITLTLGD	750
Sbjct	661	TLAKWLNLIELEFQGSGSTVQKQDVRANTAIKDIKKITLTLGD	702

> dbj|BAD00918.1| penicillin-binding protein 2X [Streptococcus pneumoniae] Length=750

Score = 1340 bits (3469), Expect = 0.0, Method: Composition-based stats.
Identities = 692/750 (92%), Positives = 718/750 (95%), Gaps = 0/750 (0%)

Query	1	MKWTKRVIRYATKNRKSPAENRRRVGKSLSSLGVFAIFLVNFAVIIGTGRFGTDLAK	60
Sbjct	1	MKWTKRVIRYATKNRKSPAENRRRVGKSLSSLGVFAIFLVNFAVIIGTGRFGTDLAK	60
Query	61	EAKKVKHQTTTRVPAKRGTIYDRNGVPIAEDATSYNVYAVIDENYKSATGKILYVEKTQFN	120
Sbjct	61	EAKKVKHQTTTRVPAKRGTIYDRNGVPIAEDATSYNVYAVIDENYKSATGKILYVEKTQFN	120
Query	121	KVAEVFKYLDMEESYVREQLSQPNLKQVSFGAKGNIGITYANMMSIKKELEAAEVKGIDF	180
Sbjct	121	KVAEVFKYLDMEESYVREQLSQPNLKQVSFGAKGNIGITYANMMSIKKELEAAEVKGIDF	180
Query	181	TTSPNRSYPNGQFASSFIGLAQLHENEDGSKSLLGTSGMESSLNSILAGTDGIITYEKDR	240
Sbjct	181	TTSPNRSYPNGQFASSFIGLAQLHENEDGSKSLLGTSGMESSLNSILAGTDGIITYEKDR	240

Query	241	LGNIVPGTEQVSQRTMDGKDVTYTTISSLPLQSFMETQMDAFQEKVKGKYMATLVSAKTGE LGNIVPGTEQVSQRTMDGKDVTYTTISSLPLQSFMETQMDAF EKVKGKYMATLVSAKTGE	300
Sbjct	241	LGNIVPGTEQVSQRTMDGKDVTYTTISSLPLQSFMETQMDAFLEKVKGKYMATLVSAKTGE	300
Query	301	ILATTQRPTFDADTKEGITEDFVWRDILYQSNEYPGSTMVKVMMAAAIDNNNTFPGEVFN ILATTQRPTF+ADTKEGITEDFVWRDILYQSNEYPGS MKVM LA++IDNNNTFP GE FN	360
Sbjct	301	ILATTQRPTFNADTKEGITEDFVWRDILYQSNEYPGSAMKVMTLASSIDNNNTFPSGEYFN	360
Query	361	SSELKIADATIRDWDVNNEGLTGGRMMTFSQGFAHSSNVGMTLLEQKMGDATWLDYLNRFK SSE KIADAT RDWDVN+GLT G MMTF QGFAHSSNVGM+LLEQKMGDATWLDYL RFK	420
Sbjct	361	SSEFKIADATTRDWDVNNDGLTGGMMTFLQGFAHSSNVGMSLLEQKMGDATWLDYLKRFK	420
Query	421	FGVPTRFGLTDEYAGQLPADNIVNIAQSSFGQGISVTQTQMIRRAFTAIANDGVMLEPKFI FGVPTRFGLTDEYAGQLPADNIV+IAQSSFGQGISVTQTQM+RAFTAIANDGVMLEPKFI	480
Sbjct	421	FGVPTRFGLTDEYAGQLPADNIVSIAQSSFGQGISVTQTQMLRAFTAIANDGVMLEPKFI	480
Query	481	SAIYDPNDQTARKSQEIVGNPVSCKDAASLTRTNMVLVGTDPVYGTMYNHSTGKPTVTVP SAIYD N+Q+ RKSQEIVGNPVSCK+AAS TR +M+LVGTDP+YGTMYNH TGKP +TVP	540
Sbjct	481	SAIYDTNNQSVRSQEIVGNPVSCKEAASTRRNHMILVGTDPYGTMYNHYTGKPIITVP	540
Query	541	GQNVALKSGTAQIADEKNGGYLVGLTDYIFSAVMSSPAENPDFILYVTVQQPEHYSGIQL GQNVA+KSGTAQIADEKNGGYLVG T+YIFS V+M+PAENPDFILYVTVQQPEHYSGIQL	600
Sbjct	541	GQNVAVKSGTAQIADEKNGGYLVGSTNYIFSVVTMNPAAENPDFILYVTVQQPEHYSGIQL	600
Query	601	GEFANPILERASAMKDSLNLQTTAKALEQVSQQSPYPMPSVKDISPGDLAELRRNLVQP GEFANPILERA AMKDSLNLQ+TAK L+QV+ QS Y MPS+KDISPGDLAE LRRN+VQP	660
Sbjct	601	GEFANPILERAVAMKDSLNLQSTAKTLQDVNTQSYAMPSIKDISPGDLAEALRRNIVQP	660
Query	661	IVVGTGTKIKNSSAEEGKNLAPNQQVLILSDKAEEVPDMYGWTKETAETLAKWLNLIEF IVVGTGTKIK SS EEG NLAPNQQVL+LSDKAEEVPDMYGWTK TAE +KWLNLIEL F	720
Sbjct	661	IVVGTGTKIKESSVEEGSNLAPNQQVLLSDKAEEVPDMYGWTKATAEAFSKWLNLIELVF	720
Query	721	QGGSTVQKQDVRANTAIKDIKKITLTLD +GGSTVQKQDVRANTAIKDIKKITLTLD	750
Sbjct	721	EGSGSTVQKQDVRANTAIKDIKKITLTLD	750

>dbj|BAD00910.1| penicillin-binding protein 2X [Streptococcus pneumoniae]
Length=750

Score = 1336 bits (3458), Expect = 0.0, Method: Composition-based stats.
Identities = 690/750 (92%), Positives = 719/750 (95%), Gaps = 0/750 (0%)

Query	1	MKWTKRVIRYATKNRKSPAENRRVGKSLSSLGVFAIFLVNFIAVIIGTGTRFGTDLAK MKWTKRVIRYATKNRKSPAENRRVGKSLSSLGVFAIFLVNFIAVIIGTGTRFGTDLAK	60
Sbjct	1	MKWTKRVIRYATKNRKSPAENRRVGKSLSSLGVFAIFLVNFIAVIIGTGTRFGTDLAK	60
Query	61	EAKKVHQTTRTVPAKRGTIYDRNGVPIAEDATSYNVYAVIDENYKSATGKILYVEKTQFN EAKKVHQTTRTVPAKRGTIYDRNGVPIAEDATSYNVYAVIDENYKSATGKILYVEKTQFN	120
Sbjct	61	EAKKVHQTTRTVPAKRGTIYDRNGVPIAEDATSYNVYAVIDENYKSATGKILYVEKTQFN	120
Query	121	KVAEVFHKLDMEESYVREQLSQPNLKQVSFGAKGNIGINITYANMMSIKKELEAAEVKGIDF KVAEVFHKLDMEESYVREQLSQPNLKQVSFGAKGNIGINITYANMMSIKKELEAAEVKGIDF	180
Sbjct	121	KVAEVFHKLDMEESYVREQLSQPNLKQVSFGAKGNIGINITYANMMSIKKELEAAEVKGIDF	180
Query	181	TTSPNRSPNGQFASSFIGLAOLHENEDGSKSLLGTSGMESLNSILAGTDGIITYEKDR TTSPNRSPNGQFASSFIGLAOLHENEDGSKSLLGTSGMESLNSILAGTDGIITYEKDR	240
Sbjct	181	TTSPNRSPNGQFASSFIGLAOLHENEDGSKSLLGTSGMESLNSILAGTDGIITYEKDR	240
Query	241	LGNIVPGTEQVSQRTMDGKDVTYTTISSLPLQSFMETQMDAFQEKVKGKYMATLVSAKTGE LGNIVPGTEQVSQRTMDGKDVTYTTISSLPLQSFMETQMDAFQEKVKGKYMATLVSAKTGE	300
Sbjct	241	LGNIVPGTEQVSQRTMDGKDVTYTTISSLPLQSFMETQMDAFQEKVKGKYMATLVSAKTGE	300
Query	301	ILATTQRPTFDADTKEGITEDFVWRDILYQSNEYPGSTMVKVMMAAAIDNNNTFPGEVFN ILATTQRPTFDADTKEGITEDFVWRDILYQSNEYPGS MKVM LA++IDNNNTFP GE FN	360
Sbjct	301	ILATTQRPTFDADTKEGITEDFVWRDILYQSNEYPGSAMKVMTLASSIDNNNTFPSGEYFN	360
Query	361	SSELKIADATIRDWDVNNEGLTGGRMMTFSQGFAHSSNVGMTLLEQKMGDATWLDYLNRFK SSE KIADAT RDWDVNNEGLT G MMTF QGFAHSSNVGM+LLEQKMGDATWLDYL RFK	420
Sbjct	361	SSEFKIADATTRDWDVNNEGLTGGMMTFLQGFAHSSNVGMSLLEQKMGDATWLDYLKRFK	420
Query	421	FGVPTRFGLTDEYAGQLPADNIVNIAQSSFGQGISVTQTQMIRRAFTAIANDGVMLEPKFI FGVPTRFGLTDEYAGQLPADNIV+IAQSSFGQGISVTQTQM+RAFTAIANDGVMLEPKFI	480
Sbjct	421	FGVPTRFGLTDEYAGQLPADNIVSIAQSSFGQGISVTQTQMLRAFTAIANDGVMLEPKFI	480
Query	481	SAIYDPNDQTARKSQEIVGNPVSCKDAASLTRTNMVLVGTDPVYGTMYNHSTGKPTVTVP SAIYD N+Q+ RKSQEIVGNPVSCK+AAS TR +M+LVGTDP+YGTMYNH TGKP +TVP	540
Sbjct	481	SAIYDTNNQSVRSQEIVGNPVSCKEAASTRRNHMILVGTDPYGTMYNHYTGKPIITVP	540
Query	541	GQNVALKSGTAQIADEKNGGYLVGLTDYIFSAVMSSPAENPDFILYVTVQQPEHYSGIQL GQNVA+KSGTAQIADEKNGGYLVG T+YIFS A+M+PAENPDFILYVTVQQPEHYSGIQL	600
Sbjct	541	GQNVAVKSGTAQIADEKNGGYLVGSTNYIFSAVTMNPAAENPDFILYVTVQQPEHYSGIQL	600
Query	601	GEFANPILERASAMKDSLNLQTTAKALEQVSQQSPYPMPSVKDISPGDLAELRRNLVQP GEFA PILERASAMK+SLNLQ+ AK L++V+ +S Y MPS+KDISPG+LAE LRRN+VQP	660
Sbjct	601	GEFATPILERASAMKESLNQSPAKNLKVTTESSYAMPSIKDISPGELAEALRRNIVQP	660

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- Query 661 I V V G T G T K I K N S S A E E G K N L A P N Q Q V L I L S D K A E E V P D M Y G W T K E T A E T L A K W L N I E L E F 720
  Sbjct 661 I V V G T G T K I K SS E E G N L A P N Q Q V L + L S D K A E E V P D M Y G W T K T A E + K W L N I E + F 720
- Query 721 Q G S G S T V Q K Q D V R A N T A I K D I K K I T L T L G D 750
  Sbjct 721 + G S G S T V Q K Q D V R A N T A I K D I K K I T L T L G D 750
  Sbjct 721 E G S G S T V Q K Q D V R A N T A I K D I K K I T L T L G D 750

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>dbj|BAD00923.1| penicillin-binding protein 2X [Streptococcus pneumoniae]
 dbj|BAD00924.1| penicillin-binding protein 2X [Streptococcus pneumoniae]
 dbj|BAD00934.1| penicillin-binding protein 2X [Streptococcus pneumoniae]
 Length=750

Score = 1327 bits (3433), Expect = 0.0, Method: Composition-based stats.
 Identities = 683/750 (91%), Positives = 716/750 (95%), Gaps = 0/750 (0%)

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Query 1 M K W T K R V I R Y A T K N R K S P A E N R R R V G K S L S L S V F V F A I F L V N F A V I I G T G T R F G T D L A K 60
  Sbjct 1 M K W T K R V I R Y A T K N R K S P A E N R R R V G K S L S L S V F V F A I F L V N F A V I I G T G T R F G T D L A K 60
Query 61 E A K K V H Q T T R T V P A K R G T I Y D R N G V P I A E D A T S Y N V Y A V I D E N Y K S A T G K I L Y V E K T Q F N 120
  Sbjct 61 E A K K V H Q T T R T V P A K R G T I Y D R N G V P I A E D A T S Y N V Y A V I D E N Y K S A T G K I L Y V E K T Q F N 120
Query 121 K V A E V F H K Y L D M E E S Y V R E Q L S Q P N L K Q V S F G A K G N G I T Y A N M M S I K K E L A A E V K G I D F 180
  Sbjct 121 K V A E V F H K Y L D M E E S Y V R E Q L S Q P N L K Q V S F G A K G N G I T Y A N M M S I K K E L A A E V K G I D F 180
Query 181 T T S P N R S Y P N G Q F A S S F I G L A Q L H E N E D G S K S L L G T S G M E S S L N S I L A G T D G I I T Y E K D R 240
  Sbjct 181 T T S P N R S Y P N G Q F A S S F I G L A Q L H E N E D G S K S L L G T S G M E S S L N S I L A G T D G I I T Y E K D R 240
Query 241 L G N I V P G T E Q V S Q R T M D G K D V Y T T I S S P L Q S F M E T Q M D A F Q E K V K G K Y M T A T L V S A K T G E 300
  Sbjct 241 L G N I V P G T E Q V S Q R T M D G K D V Y T T I S S P L Q S F M E T Q M D A F E K V K G K Y M T A T L V S A K T G E 300
Query 301 I L A T T Q R P T F D A D T K E G I T E D F V W R D I L Y Q S N Y E P G S T M K V V M M L A A I D N N T F P G G E V F N 360
  Sbjct 301 I L A T T Q R P T F + A D T K E G I T E D F V W R D I L Y Q S N Y E P G S M K V M L A + I D N N T F P G E F N 360
I L A T T Q R P T F N A D T K E G I T E D F V W R D I L Y Q S N Y E P G S A M K V M T L A S S I D N N T F P S G E Y F N 360
Query 361 S S E L K I A D A T I R D W D V N V E G L T G G R R M M T F S Q G F A H H S S N V G M T L L E Q K M G D A T W L D Y L N R F K 420
  Sbjct 361 S S E F K I A D A T T R D W D V N D G L T T G G M M T F L Q G F A H H S S N V G M S L L E Q K M G D A T W L D Y L K R F K 420
Query 421 F G V P T R F G L T D E Y A G Q L P A D N I V N I A Q S S F G Q G I S V T Q T Q M I R A F T A I A N D G V M L E P K F I 480
  Sbjct 421 F G V P T R F G L T D E Y A G Q L P A D N I V + I A Q S S F G Q G I S V T Q T Q M + R A F T A I A N D G V M L E P K F I 480
Query 481 S A I Y D P N D Q T A R K S Q K E I V G N P V S K D A A S L T R T N M V L V G T D P V Y G T M Y N H S T G K P T V T V P 540
  Sbjct 481 S A I Y D N + Q + R K S Q K E I V G N P V S K + A A S T R + M + L V G T D P + Y G T M Y N H T G K P + T V P 540
S A I Y D T N N Q S V R K S Q K E I V G N P V S K E A A S T R N H M I L V G T D P L Y G T M Y N H T G K P I I T V P 540
Query 541 G Q N V A L K S G T A Q I A D E K N G G Y L V G L T D Y I F S A V S M S P A E N P D F I L Y V T V Q Q P E H Y S G I Q L 600
  Sbjct 541 G Q N V A V K S G T A Q I A D E K N G G Y L V G S T N Y I F S V V T M N P A E N P D F I L Y V T V Q Q P E H Y S G I Q L 600
Query 601 G E F A N P I L E R A S A M K D S L N L Q T T A K A L E Q V S Q Q S P Y P M P S V K D I S P G D L A E E L R R N L V Q P 660
  Sbjct 601 G E F A P I L E R A S A M K + S L N L Q + A K L + V + + S Y M P S + K D I S P G + L A E L R R N + V Q P 660
G E F A T P I L E R A S A M K E S L N L Q S P A K N L D K V T T E S S Y A M P S I K D I S P G E L A E A L R R N I V Q P 660
Query 661 I V V G T G T K I K N S S A E E G K N L A P N Q Q V L I L S D K A E E V P D M Y G W T K E T A E T L A K W L N I E L E F 720
  Sbjct 661 I V V G T G T K I K + S E E G N L A P N Q Q V L + L S D K E E + P D M Y G W K E T A E T A K W L + I E L E F 720
I V V G T G T K I K E T S V E E G T N L A P N Q Q V L L S D K V E E I P D M Y G W K K E T A E T F A K W L D I E L E F 720
Query 721 Q G S G S T V Q K Q D V R A N T A I K D I K K I T L T L G D 750
  Sbjct 721 + G S G S V Q K Q D V R N T A I K N I K K I T L T L G D 750
  Sbjct 721 E G S G S V V Q K Q D V R T N T A I K N I K K I T L T L G D 750

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>dbj|BAD00917.1| penicillin-binding protein 2X [Streptococcus pneumoniae]
 Length=750

Score = 1324 bits (3427), Expect = 0.0, Method: Composition-based stats.
 Identities = 680/750 (90%), Positives = 717/750 (95%), Gaps = 0/750 (0%)

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Query 1 M K W T K R V I R Y A T K N R K S P A E N R R R V G K S L S L S V F V F A I F L V N F A V I I G T G T R F G T D L A K 60
  Sbjct 1 M K W T K R V I R Y A T K N R K S P A E N R R R V G K S L S L S V F V F A I F L V N F A V I I G T G T R F G T D L A K 60
Query 61 E A K K V H Q T T R T V P A K R G T I Y D R N G V P I A E D A T S Y N V Y A V I D E N Y K S A T G K I L Y V E K T Q F N 120
  Sbjct 61 E A K K V H Q T T R T V P A K R G T I Y D R N G V P I A E D A T S Y N V Y A V I D E N Y K S A T G K I L Y V E K T Q F N 120
Query 121 K V A E V F H K Y L D M E E S Y V R E Q L S Q P N L K Q V S F G A K G N G I T Y A N M M S I K K E L A A E V K G I D F 180

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- Sbjct	121	KVAEVFH KYLDMEESYVREQLSQPNLKQVSFG+KGNNGITYANMM+IKKELE AEVKGIDF KVAEVFH KYLDMEESYVREQLSQPNLKQVSFGSKGNNGITYANMMAIKKELEAEVKGIDF	180
Query	181	TTSPNRSPNGQFASSFIGLAQLHENEDEDGSKSLLGTSGMESSLNSILAGTDGIITYEKDR TTSPNRSPNGQFASSFIGLAQLHENEDEDGSKSLLGTSGMESSLNSILAGTDGIITYEKDR	240
- Sbjct	181	TTSPNRSPNGQFASSFIGLAQLHENEDEDGSKSLLGTSGMESSLNSILAGTDGIITYEKDR TTSPNRSPNGQFASSFIGLAQLHENEDEDGSKSLLGTSGMESSLNSILAGTDGIITYEKDR	240
Query	241	LGNIVPGTEQVSQRTMDGKDVTIISPLQSFMETQMDAFQEKVKGKYMTATLVSAKTGE LGNIVPGTEQVSQ+T+DGKDVTIISPLQSFMETQMDAFQEKVKGKYMTATLVSAKTGE	300
Sbjct	241	LGNIVPGTEQVSQQTVDGKDVTIISPLQSFMETQMDAFQEKVKGKYMTATLVSAKTGE LGNIVPGTEQVSQQTVDGKDVTIISPLQSFMETQMDAFQEKVKGKYMTATLVSAKTGE	300
Query	301	ILATTQRPTFDADTKEGITEDFVWRDILYQSNYEPEGSTMKVMMIAAIIDNNTFPGEVFN ILATTQRPTFDADTKEG+T+DFVWRDILYQSNYEPEGS MKVM LA++IDNNTFP GE FN	360
Sbjct	301	ILATTQRPTFDADTKEGLT KDFVWRDILYQSNYEPEGSAMKVMTLASSIDNNTFPSGEYFN ILATTQRPTFDADTKEGLT KDFVWRDILYQSNYEPEGSAMKVMTLASSIDNNTFPSGEYFN	360
Query	361	SSELKIADATIRDWDVNNEGLTGGRMMTSQGFAHSSNVGMLLEQKMGDATWLDYLNRFK SSE KIADAT RDWDVN+GLT G MMTF QGFAHSSNVGM+LLEQKMGDATWLDYL RFK	420
Sbjct	361	SSEFKIADATTRDWDVNGLTTGGMMTFLQGFAHSSNVGMSLLEQKMGDATWLDYLKRFK SSEFKIADATTRDWDVNGLTTGGMMTFLQGFAHSSNVGMSLLEQKMGDATWLDYLKRFK	420
Query	421	FGVPTRFGLTDEYAGQLPADNIVNIAQSSFGQGISVTQTMIRFTAIAANDGVMLEPKFI FGVPTRFGLTDEYAGQLPADNIV+IAQSSFGQGISVTQTM+RAFTAIANDGVMLEPKFI	480
Sbjct	421	FGVPTRFGLTDEYAGQLPADNIVSIAQSSFGQGISVTQTMIRFTAIAANDGVMLEPKFI FGVPTRFGLTDEYAGQLPADNIVSIAQSSFGQGISVTQTMIRFTAIAANDGVMLEPKFI	480
Query	481	SAIYDPNDQTARKSQKEIVGNPVS KDAASLRTNMVLVGTDPVYGTMYNHSTGKPTVTVP SAIYD N+Q+ RKSQKEIVGNPVS K+AAS TR +M+LVGTD P+YGTMYNH TGKP +TVP	540
Sbjct	481	SAIYDTNNQSVRKSQKEIVGNPVS KEAAS TR NHMILVGTDPLYGTMYNHYGKPIITVP SAIYDTNNQSVRKSQKEIVGNPVS KEAAS TR NHMILVGTDPLYGTMYNHYGKPIITVP	540
Query	541	GQNVALKSGTAQIADEKNGGYLVGLTDYIFSAVSMSPAENPDFILYVTVQQPEHYSGIQL GQNV A+KSGTAQIADEKNGGYLVG T+YIFSAV+M+PAENPDFILYVTVQQPEHYSGIQL	600
Sbjct	541	GQNVAVKSGTAQIADEKNGGYLVG STNYIFSAVTMNP AENPDFILYVTVQQPEHYSGIQL GQNVAVKSGTAQIADEKNGGYLVG STNYIFSAVTMNP AENPDFILYVTVQQPEHYSGIQL	600
Query	601	GEFANPILERASAMKDSLNLQTTAKALEQVSQQSPYPMPSVKDISPGDLAEELRRNLVQP GEFA PILERASAMK+SLNLQ+ AK L++V+ +S Y MPS+KDISPGDLAE LRRN+VQP	660
Sbjct	601	GEFATPILERASAMKESLN LQSPAKNLDKVTESSYAMPSIKDISPGDLAEALRRNIVQP GEFATPILERASAMKESLN LQSPAKNLDKVTESSYAMPSIKDISPGDLAEALRRNIVQP	660
Query	661	IVVGTGKIKKNSSAEEGKNLAPNQQLI LSDKAEEV PDMYGW KETAETLAKWL NIELEF IVVGTGKIK +S E EGK NLAPNQQL+LSDK EE+PDMYGW KETAET AKWL+IELEF	720
Sbjct	661	IVVGTGKIKETSVEEGKNLAPNQQLLSDK VEEIPDMYGW KETAETFAKWL DIELEF IVVGTGKIKETSVEEGKNLAPNQQLLSDK VEEIPDMYGW KETAETFAKWL DIELEF	720
Query	721	QGSGSTVQKQDV RANTAIKDIKKITL LGD 750 +GSGS VQKQDV RNTAIK+IKKI LTLGD	750
Sbjct	721	EGSGS VVQKQDV RNTAIKNIK KIKL LGD 750	750

>dbj|BAD00927.1| penicillin-binding protein 2X [Streptococcus pneumoniae]
Length=750

Score = 1323 bits (3425), Expect = 0.0, Method: Composition-based stats.
Identities = 681/750 (90%), Positives = 715/750 (95%), Gaps = 0/750 (0%)
Query 1 MKWTKR VIRYAT KNRK SPAEN RRRVGK SLSL SVFV FAI FLVN FAVI IGTGTRFGTDLAK MKWTKR VIRYAT KNRK SPAEN RRRVGK SLSL SVFV FAI FLVN FAVI IGTGTRFGTDLAK
Sbjct 1 MKWTKR VIRYAT KNRK SPAEN RRRVGK SLSL SVFV FAI FLVN FAVI IGTGTRFGTDLAK
Query 61 EAKK VHQT RTV PAKR GTI YDRNGVPIAEDATSYN VYAVI DENY KSATG KILY VEKTQFN EAKK VHQT RTV PAKR GTI YDRNGVPIAEDATSYN VYAVI DENY KSATG KILY VEKTQFN
Sbjct 61 EAKK VHQT RTV PAKR GTI YDRNGVPIAEDATSYN VYAVI DENY KSATG KILY VEKTQFN
Query 121 KVAEV FH KYLDMEESYVREQLSQPNLKQVSFGAKGNNGITYANMMSIKKELEAAEVKGIDF KVAEV FH KYLDMEESYVREQLSQPNLKQVSFGAKGNNGITYANMMSIKKELEAAEVKGIDF
Sbjct 121 KVAEV FH KYLDMEESYVREQLSQPNLKQVSFGAKGNNGITYANMMSIKKELEAAEVKGIDF
Query 181 TTSPNRSPNGQFASSFIGLAQLHENEDEDGSKSLLGTSGMESSLNSILAGTDGIITYEKDR TTSPNRSPNGQFASSFIGLAQLHENEDEDGSKSLLGTSGMESSLNSILAGTDGIITYEKDR
Sbjct 181 TTSPNRSPNGQFASSFIGLAQLHENEDEDGSKSLLGTSGMESSLNSILAGTDGIITYEKDR
Query 241 LGNIVPGTEQVSQRTMDGKDVTIISPLQSFMETQMDAFQE KVKGKYMTATLVSAKTGE LGNIVPGTEQVSQ+T+DGKDVTIISPLQSFMETQMDAF EKVKGKYMTATLVSAKTGE
Sbjct 241 LGNIVPGTEQVSQQTVDGKDVTIISPLQSFMETQMDAFLE KVKGKYMTATLVSAKTGE
Query 301 ILATTQRPTFDADTKEGITEDFVWRDILYQSNYEPEGSTMKVMMIAAIIDNNTFPGEVFN ILATTQRPTF+ADTKEGITEDFVWRDILYQSNYEPEGS MKVM LA++IDNNTFP GE FN
Sbjct 301 ILATTQRPTF+ADTKEGITEDFVWRDILYQSNYEPEGS MKVM LA++IDNNTFP GE FN
Query 361 SSELKIADATIRDWDVNNEGLTGGRMMTSQGFAHSSNVGMLLEQKMGDATWLDYLNRFK SSE KIADAT RDWDVNNEGLT G MMTF QGFAHSSNVGM+LLEQKMGDATWLDYL RFK
Sbjct 361 SSEFKIADATTRDWDVNGLTTGGMMTFLQGFAHSSNVGMSLLEQKMGDATWLDYLKRFK
Query 421 FGVPTRFGLTDEYAGQLPADNIVNIAQSSFGQGISVTQTMIRFTAIAANDGVMLEPKFI FGVPTRFGLTDEYAGQLPADNIV+IAQSSFGQGISVTQTM+RAFTAIANDGVMLEPKFI
Sbjct 421 FGVPTRFGLTDEYAGQLPADNIVSIAQSSFGQGISVTQTMIRFTAIAANDGVMLEPKFI
Query 481 SAIYDPNDQTARKSQKEIVGNPVS KDAASLRTNMVLVGTDPVYGTMYNHSTGKPTVTVP SAIYD N+Q+ RKSQKEIVGNPVS K+AAS TR +M+LVGTD P+YGTMYNH TGKP +TVP
Sbjct 481 SAIYDTNNQSVRKSQKEIVGNPVS KEAAS TR NHMILVGTDPLYGTMYNHYGKPIITVP

NCBI Blast:PBP2X-R6

Query	541	GQVALKSGTAQIADEKNGGYLVGLTDYIFSAVMSPAENPDFILYVTVQQPEHYSIGQL GQNVA+KSGTAQIADEKNGGYLVG T+YIFSAV+M+PAENPDFILYVTVQQPEHYSIGQL	600
Sbjct	541	GQNVAKSGTAQIADEKNGGYLVGSTNYIFSAVTMNPAAENPDFILYVTVQQPEHYSIGQL	600
Query	601	GEFANPILERASAMKDSLNLQTTAKALEQVSQQSPYPMPSVKDISPGDLAELRRNLVQP GEFA PILERASAMK+SLNLQ+ AK L++V+ +S Y MPS+KDISPGDLAELRRN+VQP	660
Sbjct	601	GEFATPILERASAMKESLNLSQSPAKNLKVTESSYAMPSIKDISPGDLAELRRNIVQP	660
Query	661	IVVGTGKIKNSSAEGKNLAPNQQVLILSDKAEEVPDMYGTWTKETAETLAKWLNLIELEF IVVG GTKIK +S EEG NLAPNQQVL+LSDK EE+PDGYGW KETAET AKWL+IELEF	720
Sbjct	661	IVVGAGTKIKETSVEEGTNLAPNQQVLLSDKVSEEIPDMYGWKKETAETFAKWL DIELEF	720
Query	721	QGGSTVQKQDVRNATAIKDIKITLTLD 750 +GSGS VQKQDVR NTAIK+IKKI LTLD	750
Sbjct	721	EGSGSVVQKQDVRTNTAIKNIKKIKLTLD 750	750

>dbj|BAD00913.1| penicillin-binding protein 2X [Streptococcus pneumoniae]
Length=750

Score = 1318 bits (3410), Expect = 0.0, Method: Composition-based stats.
Identities = 677/750 (90%), Positives = 714/750 (95%), Gaps = 0/750 (0%)

Query	1	MKWTKRVIRYATKNRSPAENRRRVGKSLSSLGVFAIFLVNFAVIIGTGRFTDLAK MKWTKRVIRYATKNRSPAENRRRVGKSLSSLGVFA+FLVNFAVIIGTGRFTDLAK	60
Sbjct	1	MKWTKRVIRYATKNRSPAENRRRVGKSLSSLGVFAVFLVNFAVIIGTGRFTDLAK	60
Query	61	EAKKVHQTRRTVPAKRGTYDRNGVPIAEDATSYNVYAVIDENYKSATGKILYVEKTQFN EAKKVHQTRRTVPAKRGTYDRNGVPIAEDATSYNVYAVIDENYKSATGKILYVEKTQFN	120
Sbjct	61	EAKKVHQTRRTVPAKRGTYDRNGVPIAEDATSYNVYAVIDENYKSATGKILYVEKTQFN	120
Query	121	KVAEVFKYLDMEESYVREQLSQPNLKQVSFGAKGNNGITYANMMSIKKELEAAEVKGIDF KVAEVFKYLDMEESYVREQLSQPNLKQVSFGAKGNNGITYANMM+IKKELE AEVKGIDF	180
Sbjct	121	KVAEVFKYLDMEESYVREQLSQPNLKQVSFGAKGNNGITYANMMAIKKELEAEVKGIDF	180
Query	181	TTSPNRSPNGQFASSFIGLAQLHENEDGSKSLLGTSGMESSLNSILAGTDGIITYEKDR TTSPNRSPNGQFASSFIGLAQLHENEDGSKSLLGTSGMESSLNSILAGDGIITYEKDR	240
Sbjct	181	TTSPNRSPNGQFASSFIGLAQLHENEDGSKSLLGTSGMESSLNSILAGKDGIITYEKDR	240
Query	241	LGNIVPGTEQVSQRTMDGKDVTIISPLQSFMETQMDAFQEKVKGKYMATTLSAKTGE LGNIVPGTEQVSQ+T+DGKDVT+SSPLQSFMETQMDAF EKVKGKYMATTLSAKTGE	300
Sbjct	241	LGNIVPGTEQVSQQTVDGKDVTIISPLQSFMETQMDAFLEKVKGKYMATTLSAKTGE	300
Query	301	ILATTQRPTFDADTKEGITEDFWRDILYQSNYEPGSTMVKVMMIAAIIDNNTFPGEVFN ILATTQRPTF+ADTKEGITEDFWRDILYQSNYEPGS MKVM LA+IDNNTFP GE FN	360
Sbjct	301	ILATTQRPTFNADTKEGITEDFWRDILYQSNYEPGSAMKVTLOSSIDNNTFPSGEYFN	360
Query	361	SSELKIADATIRDWDVNEGLTGGRMMTFSQGFAHSSNVGMILLEQKMGDTWLDYLNRK SSE KIADAT RDWDVNEGLT G MMTF QGFAHSSNVGM+LLEQKMGDTWLDYL RFK	420
Sbjct	361	SSEFKIADATTRDWDVNEGLTGGRMMTFLQGFAHSSNVGMSLLEQKMGDTWLDYLKRFK	420
Query	421	FGVPTRFGLTDEYAGQLPADNIVNIAQSSFGQGISVTQTMIRRAFTAIANDGVMLEPKFI FGVPTRFGLTDEYAGQLPADNIV+IAQSSFGQGISVTQTM+RAFTAIANDGVMLEPKFI	480
Sbjct	421	FGVPTRFGLTDEYAGQLPADNIVSIAQSSFGQGISVTQMLRAFTAIANDGVMLEPKFI	480
Query	481	SAIYDPNDQTARKSQKEIVGNPVSKDAASLRTNMVLVGTDPVYGTMYNHSTGKPTVTVP SAIYD N+Q+ RKSQKEIVGNPVS+ AAS TR +M+LVGTD+YGTMYNH TGKP +TVP	540
Sbjct	481	SAIYDTNNQSVRKSQKEIVGNPVSKEAATTRNHMILVGTDPYGTMYNHGTGKPIITVP	540
Query	541	GQVALKSGTAQIADEKNGGYLVGLTDYIFSAVMSPAENPDFILYVTVQQPEHYSIGQL GQNVA+KSGTAQIADEKNGGYLVG T+YIFSAV+M+PAENPDFILYVTVQQPEHYSIGQL	600
Sbjct	541	GQNVAKSGTAQIADEKNGGYLVGSTNYIFSAVTMNPAAENPDFILYVTVQQPEHYSIGQL	600
Query	601	GEFANPILERASAMKDSLNLQTTAKALEQVSQQSPYPMPSVKDISPGDLAELRRNLVQP GEFA PILERASAMK+SLNLQ+ AK L++V+ +S Y MPS+KDISPG+LAE LRRN+VQP	660
Sbjct	601	GEFATPILERASAMKESLNLSQSPAKNLKVTESSYAMPSIKDISPGELAEALRRNIVQP	660
Query	661	IVVGTGKIKNSSAEGKNLAPNQQVLILSDKAEEVPDMYGTWTKETAETLAKWLNLIELEF IVVGTGKIK +S EEG NLAPNQQVL+LSDK EE+PDGYGW KETAET AKWL+IELEF	720
Sbjct	661	IVVGTGKIKETSVEEGTNLAPNQQVLLSDKVSEEIPDMYGWKKETAETFAKWL DIELEF	720
Query	721	QGGSTVQKQDVRNATAIKDIKITLTLD 750 +GSGS VQKQDVR NTAIK+IKKI LTLD	750
Sbjct	721	EGSGSVVQKQDVRTNTAIKNIKKIKLTLD 750	750

>dbj|BAD00938.1| penicillin-binding protein 2X [Streptococcus pneumoniae]
Length=750

Score = 1316 bits (3407), Expect = 0.0, Method: Composition-based stats.
Identities = 676/750 (90%), Positives = 713/750 (95%), Gaps = 0/750 (0%)

Query	1	MKWTKRVIRYATKNRSPAENRRRVGKSLSSLGVFAIFLVNFAVIIGTGRFTDLAK MKWTKRVIRYATKNRSPAENRRRVGKSLSSLGVFA+FLVNFAVIIGTGRFTDLAK	60
Sbjct	1	MKWTKRVIRYATKNRSPAENRRRVGKSLSSLGVFAVFLVNFAVIIGTGRFTDLAK	60

Query	61	EAKKVHQTTTRVPAKRGTIYDRNGVPIAEDATSYNVYAVIDENYKSATGKILYVEKTQFN EAKKVHQTTTRVPAKRGTIYDRNGVPIAEDATSYNVYAVIDENYKSATGKILYVEKTQFN	120
Sbjct	61	EAKKVHQTTTRVPAKRGTIYDRNGVPIAEDATSYNVYAVIDENYKSATGKILYVEKTQFN EAKKVHQTTTRVPAKRGTIYDRNGVPIAEDATSYNVYAVIDENYKSATGKILYVEKTQFN	120
Query	121	KVAEVFHKYLDMEESYVREQLSQPNLKQVSFGAKGNNGITYANMMSIKKELEAAEVKGIDF KVAEVFHKYLDMEESYVREQLSQPNL QVSFGAKGNNGITYANMM+IKKELE AEVKGIDF	180
Sbjct	121	KVAEVFHKYLDMEESYVREQLSQPNLKQVSFGAKGNNGITYANMMAIKKELEAAEVKGIDF KVAEVFHKYLDMEESYVREQLSQPNLKQVSFGAKGNNGITYANMMAIKKELEAAEVKGIDF	180
Query	181	TTSPNRSYPNGQFASSFIGLAQLHENEDEGSKSLLGTSGMESSLNSILAGTDGIITYEKDR TTSPNRSYPNGQFASSFIGLAQLHENEDEGSKSLLGTSGMESSLNSILAGTDGIITYEKDR	240
Sbjct	181	TTSPNRSYPNGQFASSFIGLAQLHENEDEGSKSLLGTSGMESSLNSILAGTDGIITYEKDR TTSPNRSYPNGQFASSFIGLAQLHENEDEGSKSLLGTSGMESSLNSILAGTDGIITYEKDR	240
Query	241	LGNIVPGTEQVSQRTMDGKDVTISSLQSFMETQMDAFQEKVKGKYMATLVSAKTGE LGNIVPGTEQVSQ+T+DGKDVTISSLQSFMETQMDAF EKVVKGKYMATLVSAKTGE	300
Sbjct	241	LGNIVPGTEQVSQQTVDGKDVTISSLQSFMETQMDAFLEKVKGKYMATLVSAKTGE LGNIVPGTEQVSQQTVDGKDVTISSLQSFMETQMDAFLEKVKGKYMATLVSAKTGE	300
Query	301	ILATTQRPTFDADTKEGITEDFVWRDILYQSNYEPGSTMVKVMMAAAIDNNNTFPGEVFN ILATTQRPTF+ADTKEGITEDFVWRDILYQSNYEPGS KVMMMA++IDNNNTFP GE FN	360
Sbjct	301	ILATTQRPTFNADTKEGITEDFVWRDILYQSNYEPGSFKVMMALLASSIDNNNTFPSGEYFN ILATTQRPTFNADTKEGITEDFVWRDILYQSNYEPGSFKVMMALLASSIDNNNTFPSGEYFN	360
Query	361	SSELKIADATIRDWDVNNEGLTGRMMTFSQGFAHSSNVGMTLLEQKMGDATWLDYLNRFK SSE KIADAT RDWDVNNEGLT G MMTF QGFAHSSNVGM+LLEQKMGDATWLDYL RFK	420
Sbjct	361	SSEFKIADATTRDWDVNNEGLTGGMMTFLQGFAHSSNVGMSLLEQKMGDATWLDYLKRKF SSEFKIADATTRDWDVNNEGLTGGMMTFLQGFAHSSNVGMSLLEQKMGDATWLDYLKRKF	420
Query	421	FGVPTRFGLTDEYAGQLPADNIVNIAQSSFGQGISVTQTMIRAFTAIANDGVMLEPKFI FGVPTRFGLTDEYAGQLPADNIV+IAQSSFGQGISVTQTM+RAFTAIAANDGVMLEPKFI	480
Sbjct	421	FGVPTRFGLTDEYAGQLPADNIVSIAQSSFGQGISVTQTMIRAFTAIANDGVMLEPKFI FGVPTRFGLTDEYAGQLPADNIVSIAQSSFGQGISVTQTMIRAFTAIANDGVMLEPKFI	480
Query	481	SAIYDPNDQTARKSQKEIVGNPVSKDAASLRTTNMVLVGTDPVYGTMYNHSTGKPTVTVP SAIYD N+Q+ RKSQKEIVGNPVS+ AAS TR +M+LVGTD+YGTMYNH TGKP +TVP	540
Sbjct	481	SAIYDTNNQSVRKSQKEIVGNPVSKEAATTRNHMILVGTDPYGTMYNHYTGPPIITVP SAIYDTNNQSVRKSQKEIVGNPVSKEAATTRNHMILVGTDPYGTMYNHYTGPPIITVP	540
Query	541	GQNVALKSGTAQIADEKNGGYLVGLTDYIFSAVSMSPAENPDFILYVTVQQPEHYSGIQL GQNVA+KSGTAQIADEKNGGYLVG T+YIFSAV+M+PAENPDFILYVTVQQPEHYSGIQL	600
Sbjct	541	GQNVAVKSGTAQIADEKNGGYLVGSTNYIFSAVTMNPAPAENPDFILYVTVQQPEHYSGIQL GQNVAVKSGTAQIADEKNGGYLVGSTNYIFSAVTMNPAPAENPDFILYVTVQQPEHYSGIQL	600
Query	601	GEFANPILEASAMKDSLNLQTTAKALEQVQQSPYPMPSVKDIDSPGDLAELRRNLVQP GEFA PILERASAMK+SLNLQ+ AK L++V+ +S Y MPS+KDISPG+LAE LRRN+VQP	660
Sbjct	601	GEFATPILEASAMKESLNQSPAKNLDKVTESSYAMPSIKDISPGEELAEALRRNIVQP GEFATPILEASAMKESLNQSPAKNLDKVTESSYAMPSIKDISPGEELAEALRRNIVQP	660
Query	661	IVVGTGTKIKNSSAEEGKNLAPNQQVLILSDKAEEVPDMYGTWTKETAETLAKWLNLIELEF IVVGTGTKIK +S EEG NLAPNQQVL+LSDK EE+PDMDYGTWTKETAET AKWL+IELEF	720
Sbjct	661	IVVGTGTKIKETSVEEGTNLAPNQQVLLLSDKVEEI PDMDYGWKWTKETAETFAKWL DIELEF IVVGTGTKIKETSVEEGTNLAPNQQVLLLSDKVEEI PDMDYGWKWTKETAETFAKWL DIELEF	720
Query	721	QGSGSTVQKQDVRANTAIKDIIKITLTLGD 750 +GSGS VQKQDVRA NTAIK+IKKI LTLGD	750
Sbjct	721	EGSGSVVQKQDVRTNTAIKNIKKIKLTLGD 750	750

>dbj|BAD00922.1| penicillin-binding protein 2X [Streptococcus pneumoniae]
Length=750

Score = 1316 bits (3405), Expect = 0.0, Method: Composition-based stats.
Identities = 678/750 (90%), Positives = 713/750 (95%), Gaps = 0/750 (0%)

Query	1	MKWTKRVIRYATKNRSPAENRRRVGKSLSSLVFVAIFLVNFAVIIGTGTREFDLAK MKWTKRVIRYATKNRSPAENRRRVGKSLSSLVFVA+FLVNFAVIIGTGTREFDLAK	60
Sbjct	1	MKWTKRVIRYATKNRSPAENRRRVGKSLSSLVFVA+FLVNFAVIIGTGTREFDLAK MKWTKRVIRYATKNRSPAENRRRVGKSLSSLVFVA+FLVNFAVIIGTGTREFDLAK	60
Query	61	EAKKVHQTTTRVPAKRGTIYDRNGVPIAEDATSYNVYAVIDENYKSATGKILYVEKTQFN EAKKVHQTTTRVPAKRGTIYDRNGVPIAEDATSYNVYAVIDENYKSATGKILYVEKTQFN	120
Sbjct	61	EAKKVHQTTTRVPAKRGTIYDRNGVPIAEDATSYNVYAVIDENYKSATGKILYVEKTQFN EAKKVHQTTTRVPAKRGTIYDRNGVPIAEDATSYNVYAVIDENYKSATGKILYVEKTQFN	120
Query	121	KVAEVFHKYLDMEESYVREQLSQPNLKQVSFGAKGNNGITYANMMSIKKELEAAEVKGIDF KVAEVFHKYLDMEESYVREQLSQPNLKQVSFGAKGNNGITYANMMSIKKELE AEVKGIDF	180
Sbjct	121	KVAEVFHKYLDMEESYVREQLSQPNLKQVSFGAKGNNGITYANMMSIKKELEAAEVKGIDF KVAEVFHKYLDMEESYVREQLSQPNLKQVSFGAKGNNGITYANMMSIKKELEAAEVKGIDF	180
Query	181	TTSPNRSYPNGQFASSFIGLAQLHENEDEGSKSLLGTSGMESSLNSILAGTDGIITYEKDR TTSPNRSYPNGQFASSFIGLAQLHENEDEGSKSLLGTSGMESSLNSILAGTDGIITYEKDR	240
Sbjct	181	TTSPNRSYPNGQFASSFIGLAQLHENEDEGSKSLLGTSGMESSLNSILAGTDGIITYEKDR TTSPNRSYPNGQFASSFIGLAQLHENEDEGSKSLLGTSGMESSLNSILAGTDGIITYEKDR	240
Query	241	LGNIVPGTEQVSQRTMDGKDVTISSLQSFMETQMDAFQEKVKGKYMATLVSAKTGE LGNIVPGTEQVSQ+T+DGKDVTISSLQSFMETQMDAF EKVVKGKYMATLVSAKTGE	300
Sbjct	241	LGNIVPGTEQVSQQTVDGKDVTISSLQSFMETQMDAFLEKVKGKYMATLVSAKTGE LGNIVPGTEQVSQQTVDGKDVTISSLQSFMETQMDAFLEKVKGKYMATLVSAKTGE	300
Query	301	ILATTQRPTFDADTKEGITEDFVWRDILYQSNYEPGSTMVKVMMAAAIDNNNTFPGEVFN ILATTQRPTF+ADTKEGITEDFVWRDILYQSNYEPGS MKVM LA++IDNNNTFP GE FN	360
Sbjct	301	ILATTQRPTFNADTKEGITEDFVWRDILYQSNYEPGSAMKVMTLASSIDNNNTFPSGEYFN ILATTQRPTFNADTKEGITEDFVWRDILYQSNYEPGSAMKVMTLASSIDNNNTFPSGEYFN	360
Query	361	SSELKIADATIRDWDVNNEGLTGRMMTFSQGFAHSSNVGMTLLEQKMGDATWLDYLNRFK SSE KIADAT RDWDVNNEGLT G MMTF QGFAHSSNVGM+LLEQKMGDATWLDYL RFK	420
Sbjct	361	SSEFKIADATTRDWDVNNEGLTGGMMTFLQGFAHSSNVGMSLLEQKMGDATWLDYLKRKF SSEFKIADATTRDWDVNNEGLTGGMMTFLQGFAHSSNVGMSLLEQKMGDATWLDYLKRKF	420
Query	421	FGVPTRFGLTDEYAGQLPADNIVNIAQSSFGQGISVTQTMIRAFTAIANDGVMLEPKFI FGVPTRFGLTDEYAGQLPADNIV+IAQSSFGQGISVTQTM+RAFTAIAANDGVMLEPKFI	480
Sbjct	421	FGVPTRFGLTDEYAGQLPADNIVSIAQSSFGQGISVTQTMIRAFTAIANDGVMLEPKFI FGVPTRFGLTDEYAGQLPADNIVSIAQSSFGQGISVTQTMIRAFTAIANDGVMLEPKFI	480

- Query	481	SAIYDPNDQTARKSQEIVGNPVS KDAASLRT TNMVLVGTDPVY GTMYN HSTGKPTV TVP	540
Sbjct	481	SAIYD N+Q+ RKSQEIVGNPVS K+ AAS TR + M+ L VGTDP+ YGTMYN H TGKP + T VP	540
- Query	541	GQNVAL KSGTAQIADEKNGGYLVGLTDYIFSAVSM SPAENPDFILYVTVQQPEH YSGIQL	600
Sbjct	541	GQNVA+ KSGTAQIADEKNGGYLVG T+YI FSAV+ M+ PAENPDFILYVTVQQPEH YSGIQL	600
Query	601	GEFANPILERASAMKDSLNLQTTAKALEQVS QSPYPMPSVKD ISPGDLAEELRRNLVQP	660
Sbjct	601	GEFA PILERASAMK+SLNLQ+ AK L++V+ + S Y MPS+ KDISPG+ LAE LRRN+VQP	660
Query	661	IVVGTGKIKNSSAEGK NLAPNQQL LSDKAEEV PDMY GWT KETAET LAKWL NIELEF	720
Sbjct	661	IVVGTGKIK +S EEG NLAPNQQL+ LSDK EE+ PDMY GW KETAET AKWL+IELEF	720
Query	721	QGSGSTVQKQDVR RANTAI KDIKKITL LGD 750	
Sbjct	721	+GSGS VQKQDVR NTAIK+IKKI LTLGD 750	

>dbj|BAD00925.1| penicillin-binding protein 2X [Streptococcus pneumoniae]
Length=750

Score = 1315 bits (3403), Expect = 0.0, Method: Composition-based stats.
Identities = 676/750 (90%), Positives = 712/750 (94%), Gaps = 0/750 (0%)

Query	1	MKWTKRVIRYATKNR KSPAENRRVGKSL SLLSVFVFAI FLVNFAVI IGTGTRFGTDLAK	60
Sbjct	1	MKWTKRVIRYATKNR KSPAENRRVGKSL SLLSVFVFA+ FLVNFAVI IGTGTRFGTDLAK	60
Query	61	EAKKVHQ TTRVPAKRG TIYDRNGVPIAEDATSY NVYAVIDENYKSATGKILYVEKTQFN	120
Sbjct	61	EAKKVHQ TTRVPAKRG TIYDRNGVPIAEDATSY NVYAVIDENYKSATGKILYVEKTQFN	120
Query	121	KVAEVFH KYLDMEESYVRE QLSPQNLKQVS FGA KGN GITYANMMSIKKE LEAAEVKGIDF	180
Sbjct	121	KVAEVFH KYLDMEESYVRE QLSPQNLKQVS FGA KGN GITYANMMSIKKE LEAAEVKGIDF	180
Query	181	TTSPNRSPNGQFASSFIGLAQ LHENEDGSKSLLGTSGM ESSLNSIAG TDGI ITYEKDR	240
Sbjct	181	TTSPNRSPNGQFASSFIGLAQ LHENEDGSKSLLGTSGM ESSLNSIAG DGI ITYEKDR	240
Query	241	LGNIVPGTEQVS QRTMDGKD VYT TISSPLQSF METQMDA FQEKVKGKYM TATL VS AKTGE	300
Sbjct	241	LGNIVPGTEQVS Q+T+DGKD VYT+SSPLQSF METQMDA F EKVKGKYM TATL VS AKTGE	300
Query	301	ILATTQRPTFDADTKEGI TEDFVWRDIL YQS NYEPG STMKV MM LAAAIDNNTFP GGEV FN	360
Sbjct	301	ILATTQRPTF+ADTKEGI TEDFVWRDIL YQS NYEPG S KVMM LA+ IDNNTFP GE FN	360
Query	361	SSELKIA DATI RDWDVNE GLTGGRMM TFSQGF AHSN NVGM T LLEQ KMG D ATWLDYL NR FK	420
Sbjct	361	SSE KI ADAT RDWDVNE GLT G MMTF QGFAHSSNVGM+ LLEQ KMG D ATWLDYL RFK	420
Query	421	FGV PTRF GLTDEYAG QLPADN IVNIAQSSFGQG I SVT QTQ MIR AFTAI ANDGV MLEPKFI	480
Sbjct	421	FGV PTRF GLTDEYAG QLPADN IV+IAQSSFGQG I SVT QTQ M+RAFTA I ANDGV MLEPKFI	480
Query	481	SAIYDPNDQTARKSQEIVGNPVS KDAASLRT TNMVLVGTDPVY GTMYN HSTGKPTV TVP	540
Sbjct	481	SAIYD N+Q+ RKSQEIVGNPVS K+ AAS TR + M+ L VGTDP+ YGTMYN H TGKP + T VP	540
Query	541	GQNVAL KSGTAQIADEKNGGYLVGLTDYIFSAVSM SPAENPDFILYVTVQQPEH YSGIQL	600
Sbjct	541	GQNVA+ KSGTAQIADEKNGGYLVG T+YI FSAV+ M+ PAENPDFILYVTVQQPEH YSGIQL	600
Query	601	GEFANPILERASAMKDSLNLQTTAKALEQVS QSPYPMPSVKD ISPGDLAEELRRNLVQP	660
Sbjct	601	GEFA PILERASAMK+SLNLQ+ AK L++V+ + S Y MPS+ KDISPG+ LAE LRRN+VQP	660
Query	661	IVVGTGKIKNSSAEGK NLAPNQQL LSDKAEEV PDMY GWT KETAET LAKWL NIELEF	720
Sbjct	661	IVVGTGKIK +S EEG NLAPNQQL+ LSDK EE+ PDMY GW KETAET AKWL+IELEF	720
Query	721	QGSGSTVQKQDVR RANTAI KDIKKITL LGD 750	
Sbjct	721	+GSGS VQKQDVR NTAIK+IKKI LTLGD 750	

>dbj|BAD00926.1| penicillin-binding protein 2X [Streptococcus pneumoniae]
Length=750

Score = 1315 bits (3402), Expect = 0.0, Method: Composition-based stats.
Identities = 676/750 (90%), Positives = 714/750 (95%), Gaps = 0/750 (0%)

- Query	1	MKWTKRVIYATKNRSPAENRRRVGKSLSSVVFVFAIFLVNFAVIIGTGTRFGTDLAK	60
Sbjct	1	MKWTKRVIYATKNRSPAENRRRVGKSLSSVVFVFA+FLVNFAVIIGTGTRFGTDLAK	60
- Query	61	EAKKVHQTRTVPAKRGTIYDRNGVPIAEDATSYNVYAVIDENYKSATGKILYVEKTQFN	120
Sbjct	61	EAKKVHQTRTVPAKRGTIYDRNGVPIAEDATSYNVYAVIDENYKSATGKILYVEKTQFN	120
Query	121	KVAEVFHKLDMEESYVREQLSQPNLKQVSFGAKGNIGINANMMSIKKELEAAEVKGIDF	180
Sbjct	121	KVAEVFHKLDMEESYVREQLSQPNLKQVSFGAKGNIGINANMMSIKKELEAEVGKIDF	180
Query	181	TTSPNRSPNGQFASSFIGLAQLHENEDGSKSLLGTSGMESSLNSILAGTDGIITYEKDR	240
Sbjct	181	TTSPNRSPNGQFASSFIGLAQLHENEDGSKSLLGTSGMESSLNSILAGTDGIITYEKDR	240
Query	241	LGNIVPGTEQVSORTMDGKDVTIISPLQSFMETQMDAFQEKVKGKYMATTLSAKTGE+GNIVPGTE VSQ+T+DGKDVTIISPLQSFMETQMDAF EKVKGKYMATTLSAKTGE	300
Sbjct	241	VGNIVPGTELVSQQTVDGKDVTIISPLQSFMETQMDAFLEKVKGKYMATTLSAKTGE	300
Query	301	ILATTQRPTFDADTKEGITEDFVWRDILYQSNYEPGSTMVKVMMIAAIIDNNTFPGEVFN	360
Sbjct	301	ILATTQRPTF+ADTKEGITEDFVWRDILYQSNYEPGS MKVM LA++IDNNTFP GE FN	360
Query	361	SSELKIADATIRDWDVNEGTLGGRMMTFSQGFAHSSNVGMTLLEQKMGDATWLDYLNRFK	420
Sbjct	361	SSE KIADAT RDWDVNEGGLT G MMTF QGFAHSSNVGM+LLEQKMGDATWLDYL RFK	420
Query	421	FGVPTRFGLTDEYAGQLPADNIVNIAQSSFGQGISVTQTMIRAFTAIANDGVMLEPKFI	480
Sbjct	421	FGVPTRFGLTDEYAGQLPADNIV+IAQSSFGQGISVTQTM+RAFTAIANDGVMLEPKFI	480
Query	481	SAIYDPNDQTARKSQKEIVGNPVSKAASLRTTNMVLVGTDPVYGTMYNHSTGKPTVTVP	540
Sbjct	481	SAIYD N+Q+ RKSQKEIVGNPVS+AASTR +M+LVGTDP+YGTMYNH TGKP +TV	540
Query	541	GQNVALKSGTAQIADEKNGGYLVGLTDYIFSAVSMSPAENPDFILYVTVQQPEHYSGIQL	600
Sbjct	541	GQNVAVKSGTAQIADEKNGGYLVG STNYIFSAVTMNP AENPDFILYVTVQQPEHYSGIQL	600
Query	601	GEFANPILERASAMKDSLNLQTTAKALEQVSQQSPYPMPSVKDISPGDAAELRRNLVQP	660
Sbjct	601	GEFA PILERASAMK+SLNLO+ AK L++V+ +S Y MPS+KDISPG+LAE LRRN+VQP	660
Query	661	IVVGTGKIKNSSAEEGKNLAPNQQVLILSDKAEEVPMYGTWTKETAETLAKWLNLIELEF	720
Sbjct	661	IVVGTGKIK+S EEG NLAPNQQVL+LSDK EE+PMYGTWTKETAET AKWL+IELEF	720
Query	721	QGSGSTVQKQDVRA NTAIKDIKKITLTLD 750	
Sbjct	721	+GSGS VQKQDVRA NTAIK+IKKI LTLD	
		EGSGSVVQKQDVRTNTAIKNIKKIKLTLD 750	

>gb|AAF17268.1|AF210758_1 penicillin-binding protein 2X [Streptococcus pneumoniae]
Length=750

Score = 1313 bits (3398), Expect = 0.0, Method: Composition-based stats.
Identities = 675/750 (90%), Positives = 713/750 (95%), Gaps = 0/750 (0%)

Query	1	MKWTKRVIYATKNRSPAENRRRVGKSLSSVVFVFAIFLVNFAVIIGTGTRFGTDLAK	60
Sbjct	1	MKWTKRVIYATKNRSPAENRRRVGKSLSSVVFVFAIFLVNFAVIIGTGTRFGTDLAK	60
Query	61	EAKKVHQTRTVPAKRGTIYDRNGVPIAEDATSYNVYAVIDENYKSATGKILYVEKTQFN	120
Sbjct	61	EAKKVHQTRTVPAKRGTIYDRNGVPIAEDATSYNVYAVIDENYKSATGKILYVEKTQFN	120
Query	121	KVAEVFHKLDMEESYVREQLSQPNLKQVSFGAKGNIGINANMMSIKKELEAAEVKGIDF	180
Sbjct	121	KVAEVFHKLDMEESYVREQLSQPNLKQVSFG+KGNIGINANMMSIKKELEAEVGKIDF	180
Query	181	TTSPNRSPNGQFASSFIGLAQLHENEDGSKSLLGTSGMESSLNSILAGTDGIITYEKDR	240
Sbjct	181	TTSPNRSPNGQFASSFIGLAQLHENEDGSKSLLGTSGMESSLNSILAGTDGIITYEKDR	240
Query	241	LGNIVPGTEQVSORTMDGKDVTIISPLQSFMETQMDAFQEKVKGKYMATTLSAKTGE+GNIVPGTE VSQ+T+DGKDVTIISPLQSFMETQMDAF EKVKGKYMATTLSAKTGE	300
Sbjct	241	VGNIVPGTELVSQQTVDGKDVTIISPLQSFMETQMDAFLEKVKGKYMATTLSAKTGE	300
Query	301	ILATTQRPTFDADTKEGITEDFVWRDILYQSNYEPGSTMVKVMMIAAIIDNNTFPGEVFN	360
Sbjct	301	ILATTQRPTF+ADTKEGITEDFVWRDILYQSNYEPGS MKVM LA++IDNNTFP GE FN	360
Query	361	SSELKIADATIRDWDVNEGTLGGRMMTFSQGFAHSSNVGMTLLEQKMGDATWLDYLNRFK	420
		SSE KIADAT RDWDVNEGGLT G MMTF QGFAHSSNVGM+LLEQKMGDATWLDYL RFK	

NCBI Blast:PBP2X-R6

Sbjct	361	SSEFKIADATTRDWDVNDGLTGGMMTFLQGFAHSSNVGMSLLEQKMGDATWLDYLRKF	420
Query	421	FGVPTRFGLTDEYAGQLPADNIVNIAQSSFGQGISVTQTQMIRAFATAIANDGVMLEPKFI	480
Sbjct	421	FGVPTRFGLTDEYAGQLPADNIV+IAQSSFGQGISVTQTQM+RAFTAIAANDGVMLEPKFI	480
Query	481	SAIYDPNDQTARKSQEIVGNPVSCKDAASLRTNMVLVGTDPVYGTMYNHSTGKPTVTVP SAIYD N+Q+ RKSQEIVGNPVSCK+AAS TR +M+LVGTD+YGTMYNH TGKP +TVP	540
Sbjct	481	SAIYDTNNQSVRKSQEIVGNPVSCKEAASSTRNHMILVGTDPYGTMYNHSTGKPIITVP	540
Query	541	GQNVALKSGTAQIADEKNGGYLVGLTDYIFSAVSMSPAENPDFILYVTVQQPEHYSGIQL	600
Sbjct	541	GQNVA+KSGTAQIADEKNGGYLVG T+YIFS V+M+PAENPDFILYVTVQQPEHYSGIQL	600
Query	601	GEFANPILEASAMKDSLNLQTTAKALEQVSQQSPYPMPSVKDISPGDLAELRRNLVQP	660
Sbjct	601	GEFA PILERASAMK+SLNLQ+ AK L++V+ +S Y MPS+KDISPG+LAE LRRN+VQP	660
Query	661	IVVGTGKIK+S EEG NLAPNQQVL+LSDK EE+PDMYGW KETAET AKWL+IELEF	720
Sbjct	661	IVVGTGKIKETSVEEGTNLAPNQQVLLSDKVEEI PDMYGWKKETAETFAKWLDIELEF	720
Query	721	QGSGSTVQKQDVRANTAIKDIKKITL LGD 750	
Sbjct	721	+GSGS VQKQDVR NTAIK+IKKI LTLGD 750	
Sbjct	721	EGSGSVVQKQDVRTNTAIKNIKKIKL LGD 750	

>gb|AAF17270.1|AF210760_1 penicillin-binding protein 2X [Streptococcus pneumoniae]
Length=750

Score = 1312 bits (3396), Expect = 0.0, Method: Composition-based stats.
Identities = 673/750 (89%), Positives = 713/750 (95%), Gaps = 0/750 (0%)

Query	1	MKWTKRVIKYATKNRSPAENRRRVGKSLSSL SVFVFAIFLVNFAVIIGTGTRFGTDLAK	60
Sbjct	1	MKWTKKVIKYATKNRSPAENRRRVGKSLSSL SVFVFAVFLVNFAVIIGTGTRFGTDLAK	60
Query	61	EAKKVHQTRTVPAKRGTIYDRNGVPIAEDATS NVYAVIDENYKSATGKILYVEKTQFN	120
Sbjct	61	EAKKVHQTRTVPAKRGTIYDRNGVPIAEDATS NVYAVIDENYKSATGKILYVEKTQFN	120
Query	121	KVAEVFH KYLDMEESYVREQLSQPNLKQVSFGAKGN GITYANMMSIKKELEAAEVKGIDF	180
Sbjct	121	KVAEVFH KYLDMEESYVREQLSQPNLKQVSFGAKGN GITYANMM+IKKELE AEVKGIDF	180
Query	181	TTSPNRSPNGQFASSFIGLAQLHENEDGSKSLLG TSGMESSLNSILAGTDGIITYEKDR	240
Sbjct	181	TTSPNRSPNGQFASSFIGLAQLHENEDGSKSLLG TSGMESSLNSILAGTDGIITYEKDR	240
Query	241	LGNIVPGTEQVSQRTMDGKD VYTTSPLQSF METQMDAFQEKVKGKYM TATL VS AKTGE	300
Sbjct	241	LGNIVPGTEQVSQ+T+DGKDVYT+SSPLQSF METQMDAF EKVVKGKYM TATL VS AKTGE	300
Query	301	ILATTQRPTFDADTKEGITEDFVWRDILYQSN YEPGSTMVKVMM LAAAIDNNTFPGEVFN	360
Sbjct	301	ILATTQRPTF+ADTKEGITEDFVWRDILYQSN YEPGS MKVM LA++IDNNTFP GE FN	360
Query	361	SSELKIA DATIRDWDVNNEGLTGGRMMTFSQGFAHSSNVGM TLEQKMGDATWLDYLNRFK	420
Sbjct	361	SSE KIADAT RDWDVN+GLT G MMTF QGFAHSSNVGM+LLEQKMGDATWLDYL RFK	420
Query	421	FGVPTRFGLTDEYAGQLPADNIVNIAQSSFGQGISVTQTQMIRAFATAIANDGVMLEPKFI	480
Sbjct	421	FGVPTRFGLTDEYAGQLPADNIV+IAQSSFGQGISVTQTQM+RAFTAIAANDGVMLEPKFI	480
Query	481	SAIYDPNDQTARKSQEIVGNPVSCKDAASLRTNMVLVGTDPVYGTMYNHSTGKPTVTVP SAIYD N+Q+ RKSQEIVGNPVSCK+AAS TR +M+LVGTD+YGTMYNH TGKP +TVP	540
Sbjct	481	SAIYDTNNQSVRKSQEIVGNPVSCKEAASSTRNHMILVGTDPYGTMYNHSTGKPIITVP	540
Query	541	GQNVALKSGTAQIADEKNGGYLVGLTDYIFSAVSMSPAENPDFILYVTVQQPEHYSGIQL	600
Sbjct	541	GQNVA+KSGTAQIADEKNGGYLVG T+YIFS V+M+PAENPDFILYVTVQQPEHYSGIQL	600
Query	601	GEFANPILEASAMKDSLNLQTTAKALEQVSQQSPYPMPSVKDISPGDLAELRRNLVQP	660
Sbjct	601	GEFA PILERASAMK+SLNLQ+ AK L++V+ +S Y MPS+KDISPG++AE LRRN+VQP	660
Query	661	IVVGTGKIK+S EEG NLAPNQQVL+LSDK EE+PDMYGW KETAET AKWL+IELEF	720
Sbjct	661	IVVGTGKIKETSVEEGTNLAPNQQVLLSDKVEEI PDMYGWKKETAETFAKWLDIELEF	720
Query	721	QGSGSTVQKQDVRANTAIKDIKKITL LGD 750	
Sbjct	721	+GSGS VQKQDVR NTAIK+IKKI LTLGD 750	

NCBI Blast:PBP2X-R6

>dbj|BAD00932.1| penicillin-binding protein 2X [Streptococcus pneumoniae]
Length=750

Score = 1312 bits (3396), Expect = 0.0, Method: Composition-based stats.
Identities = 673/750 (89%), Positives = 712/750 (94%), Gaps = 0/750 (0%)

Query 1	MKWTKRIVYATKNRSPAENRRVGKSLSSVVFVFAIFLVNFAVIIGTGTRGTDLAK MKWTKRIVYATKNRSPAENRRVGKSLSSVVFVFA+FLVNFAVIIGTGTRGTDLAK MKWTKRIVYATKNRSPAENRRVGKSLSSVVFVFAVFLVNFAVIIGTGTRGTDLAK	60
Query 61	EAKKVHQTRTVPAKRGTIYDRNGVPIAEDATSYNVYAVIDENYKSATGKILYVEKTQFN EAKKVHQTRTVPAKRGTIYDRNGVPIAEDATSYNVYAVIDENYKSATGKILYVEKTQFN EAKKVHQTRTVPAKRGTIYDRNGVPIAEDATSYNVYAVIDENYKSATGKILYVEKTQFN	120
Sbjct 61	EAKKVHQTRTVPAKRGTIYDRNGVPIAEDATSYNVYAVIDENYKSATGKILYVEKTQFN EAKKVHQTRTVPAKRGTIYDRNGVPIAEDATSYNVYAVIDENYKSATGKILYVEKTQFN EAKKVHQTRTVPAKRGTIYDRNGVPIAEDATSYNVYAVIDENYKSATGKILYVEKTQFN	120
Query 121	KVAEVFKYLDMEESYVREQLSQPNLKQVSFGAKGNIGINANMMSIKKELEAAEVKGIDF KVAEVFKYLDMEESYVREQLSQPNLKQVSFGAKGNIGINANMMSIKKELEAAEVKGIDF KVAEVFKYLDMEESYVREQLSQPNLKQVSFGAKGNIGINANMMSIKKELEAAEVKGIDF	180
Sbjct 121	KVAEVFKYLDMEESYVREQLSQPNLKQVSFGAKGNIGINANMMSIKKELEAAEVKGIDF KVAEVFKYLDMEESYVREQLSQPNLKQVSFGAKGNIGINANMMSIKKELEAAEVKGIDF KVAEVFKYLDMEESYVREQLSQPNLKQVSFGAKGNIGINANMMSIKKELEAAEVKGIDF	180
Query 181	TTSPNRSPNGQFASSFIGLAQLHENEDGSKSLLGTSGMESSLNSILAGTDGIITYEKDR TTSPNRSPNGQFASSFIGLAQLHENEDGSKSLLGTSGMESSLNSILAGTDGIITYEKDR TTSPNRSPNGQFASSFIGLAQLHENEDGSKSLLGTSGMESSLNSILAGTDGIITYEKDR	240
Sbjct 181	TTSPNRSPNGQFASSFIGLAQLHENEDGSKSLLGTSGMESSLNSILAGTDGIITYEKDR TTSPNRSPNGQFASSFIGLAQLHENEDGSKSLLGTSGMESSLNSILAGTDGIITYEKDR TTSPNRSPNGQFASSFIGLAQLHENEDGSKSLLGTSGMESSLNSILAGTDGIITYEKDR	240
Query 241	LGNIVPGTEQVSQRTMDGKDVTYTISPLQSFMETQMDAFQEVKVKGKYMATTLSAKTGE LGNIVPGTEQVSQ+T+DGKDVTYT+SSPLQSFMETQMDAF EKVKGKYMATTLSAKTGE LGNIVPGTEQVSQQTVDGKDVTYTTLSSPLQSFMETQMDAFLEVKVKGKYMATTLSAKTGE	300
Sbjct 241	LGNIVPGTEQVSQRTMDGKDVTYTISPLQSFMETQMDAFQEVKVKGKYMATTLSAKTGE LGNIVPGTEQVSQ+T+DGKDVTYT+SSPLQSFMETQMDAF EKVKGKYMATTLSAKTGE LGNIVPGTEQVSQQTVDGKDVTYTTLSSPLQSFMETQMDAFLEVKVKGKYMATTLSAKTGE	300
Query 301	ILATTQRPTFDADTKEGITEDFVWRDILYQSNYEPGSTMVKVMMIAAIIDNNTFPGEVFN ILATTQRPTF+ADTKEGITEDFVWRDILYQSNYEPGS KVVMMLA++IDNNTFP GE FN ILATTQRPTFNADTKEGITEDFVWRDILYQSNYEPGSASFVKVMMIASSIDNNTFPSGEYFN	360
Sbjct 301	ILATTQRPTFDADTKEGITEDFVWRDILYQSNYEPGSTMVKVMMIAAIIDNNTFPGEVFN ILATTQRPTF+ADTKEGITEDFVWRDILYQSNYEPGS KVVMMLA++IDNNTFP GE FN ILATTQRPTFNADTKEGITEDFVWRDILYQSNYEPGSASFVKVMMIASSIDNNTFPSGEYFN	360
Query 361	SSELKIADATIRDWDVNEGLTGGRMMTFSQGFAQHSSNVGMLLEQKMGDATWLDPYLNRFK SSE KIADAT RDWDVNEGLT G MMTF QGFAQHSSNVGM+LLEQKMGDATWLDPYLNRFK SSEFKIADATTRDWDVNEGLTGGMMTFLQGFAQHSSNVGMSLLEQKMGDATWLDPYLNRFK	420
Sbjct 361	SSE KIADAT RDWDVNEGLT G MMTF QGFAQHSSNVGM+LLEQKMGDATWLDPYLNRFK SSEFKIADATTRDWDVNEGLTGGMMTFLQGFAQHSSNVGMSLLEQKMGDATWLDPYLNRFK	420
Query 421	FGVPTRFGLTDEYAGQLPADNIVNIAQSSFGQGQISVTOTOMIRAFTAIANDGVMLEPKFI FGVPTRFGLTDEYAGQLPADNIV+IAQSSFGQGQISVTOTOMIRAFTAIANDGVMLEPKFI FGVPTRFGLTDEYAGQLPADNIVSIAQSSFGQGQISVTOTOMIRAFTAIANDGVMLEPKFI	480
Sbjct 421	FGVPTRFGLTDEYAGQLPADNIVNIAQSSFGQGQISVTOTOMIRAFTAIANDGVMLEPKFI FGVPTRFGLTDEYAGQLPADNIV+IAQSSFGQGQISVTOTOMIRAFTAIANDGVMLEPKFI FGVPTRFGLTDEYAGQLPADNIVSIAQSSFGQGQISVTOTOMIRAFTAIANDGVMLEPKFI	480
Query 481	SAIYDPNDQTARKSQKEIVGNPVSCKDAASLRTTNMVLVGTDPVYGTMYNHSTGKPTVTVP SAIYD N+Q+ RKSQKEIVGNPVSCK+AAS TR +M+LVGTDP+YGTMYNH TGKP +TVP SAIYDTNNQSVRSQKEIVGNPVSKEAASSTTRNHMILVGTDPYGTMYNHSTGKPTVTVP	540
Sbjct 481	SAIYDPNDQTARKSQKEIVGNPVSCKDAASLRTTNMVLVGTDPVYGTMYNHSTGKPTVTVP SAIYD N+Q+ RKSQKEIVGNPVSCK+AAS TR +M+LVGTDP+YGTMYNH TGKP +TVP SAIYDTNNQSVRSQKEIVGNPVSKEAASSTTRNHMILVGTDPYGTMYNHSTGKPTVTVP	540
Query 541	GQNVALKSGTAQIADEKNGGYLVGLTDYIFSAVSMSPAENPDFILYVTVQQPEHYSGIQL GQNVVA+KSGTAQIADEKNGGYLVG T+YIFS V+M+ PAENPDFILYVTVQQPEH + +QL GQNVAVKSGTAQIADEKNGGYLVGSTNYIFSVVTMNP AENPDFILYVTVQQPEHITSVQL	600
Sbjct 541	GQNVALKSGTAQIADEKNGGYLVGLTDYIFSAVSMSPAENPDFILYVTVQQPEHYSGIQL GQNVVA+KSGTAQIADEKNGGYLVG T+YIFS V+M+ PAENPDFILYVTVQQPEH + +QL GQNVAVKSGTAQIADEKNGGYLVGSTNYIFSVVTMNP AENPDFILYVTVQQPEHITSVQL	600
Query 601	GEFANPILERASAMKDSLNLQTTAKALEQVSSQQSPYPMPSVKDISPGDLAEELRRNLVQP GEF+NPLIERASAMK+SLNLQ+ AK L++V+ +S Y MPS+KDISPG+LAE LRRN+VQP GEFSNPLIERASAMKESLNQSPAKNLKVTESSYAMPSIKDIISPGELAEALRRNIVQP	660
Sbjct 601	GEFANPILERASAMKDSLNLQTTAKALEQVSSQQSPYPMPSVKDISPGDLAEELRRNLVQP GEF+NPLIERASAMK+SLNLQ+ AK L++V+ +S Y MPS+KDISPG+LAE LRRN+VQP GEFSNPLIERASAMKESLNQSPAKNLKVTESSYAMPSIKDIISPGELAEALRRNIVQP	660
Query 661	IVVGTGKIKNSSAEEGKNLAPNQQLIILSDKAEEVPDMYGWTKETAETLAKWLNLIELEF IVVGTGKIK +S EEG NLAPNQQL+LSDK EE+PDGYW KETAET AKWL+IELEF IVVGTGKIKETSVEEGTNAPNQQLLSDKVEEI PDGYGW KETAETFAKWL DIELEF	720
Sbjct 661	IVVGTGKIKNSSAEEGKNLAPNQQLIILSDKAEEVPDMYGWTKETAETLAKWLNLIELEF IVVGTGKIK +S EEG NLAPNQQL+LSDK EE+PDGYW KETAET AKWL+IELEF IVVGTGKIKETSVEEGTNAPNQQLLSDKVEEI PDGYGW KETAETFAKWL DIELEF	720
Query 721	QGSGSTVQKQDVRANTAIDIKKITLTG 750 +GSGS VQKQDVR NTAIK+IKKI LTG 750 EGSGSVVQKQDVRTNTAIKNIKKIKLTG 750	750
Sbjct 721	QGSGSTVQKQDVRANTAIDIKKITLTG 750 +GSGS VQKQDVR NTAIK+IKKI LTG 750 EGSGSVVQKQDVRTNTAIKNIKKIKLTG 750	750

>gb|AAF17269.1|AF210759_1 penicillin-binding protein 2X [Streptococcus pneumoniae]
Length=750

Score = 1312 bits (3395), Expect = 0.0, Method: Composition-based stats.
Identities = 674/750 (89%), Positives = 712/750 (94%), Gaps = 0/750 (0%)

Query 1	MKWTKRIVYATKNRSPAENRRVGKSLSSVVFVFAIFLVNFAVIIGTGTRGTDLAK MKWTKRIVYATKNRSPAENRRVGKSLSSVVFVFA+FLVNFAVIIGTGTRGTDLAK MKWTKRIVYATKNRSPAENRRVGKSLSSVVFVFAVFLVNFAVIIGTGTRGTDLAK	60
Query 61	EAKKVHQTRTVPAKRGTIYDRNGVPIAEDATSYNVYAVIDENYKSATGKILYVEKTQFN EAKKVHQTRTVPAKRGTIYDRNGVPIAEDATSYNVYAVIDENYKSATGKILYVEKTQFN EAKKVHQTRTVPAKRGTIYDRNGVPIAEDATSYNVYAVIDENYKSATGKILYVEKTQFN	120
Sbjct 61	EAKKVHQTRTVPAKRGTIYDRNGVPIAEDATSYNVYAVIDENYKSATGKILYVEKTQFN EAKKVHQTRTVPAKRGTIYDRNGVPIAEDATSYNVYAVIDENYKSATGKILYVEKTQFN EAKKVHQTRTVPAKRGTIYDRNGVPIAEDATSYNVYAVIDENYKSATGKILYVEKTQFN	120
Query 121	KVAEVFKYLDMEESYVREQLSQPNLKQVSFGAKGNIGINANMMSIKKELEAAEVKGIDF KVAEVFKYLDMEESYVREQLSQPNLKQVSFGAKGNIGINANMMSIKKELEAAEVKGIDF KVAEVFKYLDMEESYVREQLSQPNLKQVSFGAKGNIGINANMMSIKKELEAAEVKGIDF	180
Sbjct 121	KVAEVFKYLDMEESYVREQLSQPNLKQVSFGAKGNIGINANMMSIKKELEAAEVKGIDF KVAEVFKYLDMEESYVREQLSQPNLKQVSFGAKGNIGINANMMSIKKELEAAEVKGIDF KVAEVFKYLDMEESYVREQLSQPNLKQVSFGAKGNIGINANMMSIKKELEAAEVKGIDF	180
Query 181	TTSPNRSPNGQFASSFIGLAQLHENEDGSKSLLGTSGMESSLNSILAGTDGIITYEKDR TTSPNRSPNGQFASSFIGLAQLHENEDGSKSLLGTSGMESSLNSILAGTDGIITYEKDR TTSPNRSPNGQFASSFIGLAQLHENEDGSKSLLGTSGMESSLNSILAGTDGIITYEKDR	240
Sbjct 181	TTSPNRSPNGQFASSFIGLAQLHENEDGSKSLLGTSGMESSLNSILAGTDGIITYEKDR TTSPNRSPNGQFASSFIGLAQLHENEDGSKSLLGTSGMESSLNSILAGTDGIITYEKDR TTSPNRSPNGQFASSFIGLAQLHENEDGSKSLLGTSGMESSLNSILAGTDGIITYEKDR	240
Query 241	LGNIVPGTEQVSQRTMDGKDVTYTISPLQSFMETQMDAFQEVKVKGKYMATTLSAKTGE LGNIVPGTEQVSQ+T+DGKDVTYT+SSPLQSFMETQMDAF EKVKGKYMATTLSAKTGE LGNIVPGTEQVSQQTVDGKDVTYTTLSSPLQSFMETQMDAFLEVKVKGKYMATTLSAKTGE	300
Sbjct 241	LGNIVPGTEQVSQRTMDGKDVTYTISPLQSFMETQMDAFQEVKVKGKYMATTLSAKTGE LGNIVPGTEQVSQ+T+DGKDVTYT+SSPLQSFMETQMDAF EKVKGKYMATTLSAKTGE LGNIVPGTEQVSQQTVDGKDVTYTTLSSPLQSFMETQMDAFLEVKVKGKYMATTLSAKTGE	300
Query 301	ILATTQRPTFDADTKEGITEDFVWRDILYQSNYEPGSTMVKVMMIAAIIDNNTFPGEVFN	360

NCBI Blast:PBP2X

- Sbjct	301	ILATTQRPTF+ADTKEGITEDFVWRDILYQSNYEPGS KVM LA++IDNNTFP GE FN ILATTQRPTFNADTKEGITEDFVWRDILYQSNYEPGS AFK VMT LASS IDNNTFP SGEYFN	360
Query	361	SSELKIADATIRDWDVNNEGLTGGRMMTFSQGFAHSSNVGM TLLEQKMGDATWLDYLNRFK SSE KIADAT RDWDVN GLT G MMTF SQGFAHSSNVG +LLEQKMGDATWLDYL RFK	420
- Sbjct	361	SSEFKIADATTRDWDVNAGLTTGGM MTF SQGFAHSSNVGTSLLEQKMGDATWLDYLKR FK	420
Query	421	FGVPTRFGLTDEYAGQLP ADNIVNIAQSSFGQG ISVTQTQMIRAF TAI ANDGVML EPKFI FGVPTRFGLTDEYAGQLP ADNIV +IAQSSFGQG ISVTQTQM+RAFTAI ANDGVML EPKFI	480
Sbjct	421	FGVPTRFGLTDEYAGQLP ADNIVSIAQSSFGQG ISVTQTQMRLRAFTAI ANDGVML EPKFI	480
Query	481	SAIYDPNDQTARKS QKE I VGNPVS KDAASLRT NMVL VGTDPV YGTM NHSTG KPTV TVP SAIYD N+Q+ RKS QKE I VGNPVS K+AAS TR +M+LV GTDP+Y GTM NH TGKP +TVP	540
Sbjct	481	SAIYDTNNQSGRK S QKE I VGNPVS KEAAS TR NHM ILVG TDPL YGTM NH YTG KPIITV P	540
Query	541	GQNVAL KSGTAQ IADEKNGGYLVGLTDYIFSAVSM SPAENPDF ILYVTVQ QPEHSGIQL GQNVA+KSGTAQ IADEKNGGYLVG T+YIFS V+M+PAENPDF ILYVTVQ QPEH+SGIQL	600
Sbjct	541	GQNVAVKSGTAQ IADEKNGGYLVG STNY IF SVT VMN PAENPDF ILYVTVQ QPEH FSGIQL	600
Query	601	GEFANPILERASAMKDSLNLQTTAKALEQV SQQSPYPMPSVKD ISPGD LAEELRRN L VQP GEFA PILERASAMK+SLNLQ+ AK L++V+ +S Y MPS+KDISPG+LAE LRRN+VQP	660
Sbjct	601	GEFATPILERASAMKESLN LQSPAKNLDKV TESSYAMPSIKDISPGELAEALRRNIV QP	660
Query	661	IVVGTGTKIKNSSAEEGKNLAPNQQLILSDKAEEV PDMYGW T KETAETLA KWLNIELEF IVVGTGTKIK +S EEG NLAPNQQL+LSDK EE+PDMYGW KETAET AKWL+IELEF	720
Sbjct	661	IVVGTGTKIKETSVEEGTNLAPNQQLLSDKV EEI PDMYGW KETAETFAKWL DIELEF	720
Query	721	QGSGSTVQKQDVR RANTAI KDIKKITLT LGD 750 +GSGS VQKQDVR NTAIK+IKKI LT LGD	750
Sbjct	721	EGSGSVVQKQDVRTNTAIKNIKKIKLT LGD 750	750

>dbj|BAD00936.1| penicillin-binding protein 2X [Streptococcus pneumoniae]
Length=750

Score = 1312 bits (3395), Expect = 0.0, Method: Composition-based stats.
Identities = 675/750 (90%), Positives = 712/750 (94%), Gaps = 0/750 (0%)

Query	1	MKWTKRVIRYATKNR KSPAENRR RVGKSL SLLS VFVFAI FLVN FAIVI IGTGTRG TD LAK MKWTKRVIRYATKNR KSPAENRR RVGKSL SLLS VFVFA+FLVN FAIVI IGTGTRG TD LAK	60
Sbjct	1	MKWTKRVIRYATKNR KSPAENRR RVGKSL SLLS VFVFAVFLVN FAIVI IGTGTRG TD LAK	60
Query	61	EAKKVHQ TTRVPAKRG TIYDRNGVPIAEDATSY NVYAVI DENYKS ATGK ILYVEKTQFN EAKKVHQ TTR VPAKRG TIYDRNGVPIAEDATSY NVYAVI DENYKS ATGK ILYVEKTQFN	120
Sbjct	61	EAKKVHQ TTRVPAKRG TIYDRNGVPIAEDATSY NVYAVI DENYKS ATGK ILYVEKTQFN	120
Query	121	KVAEVFH KYLDMEESYVRE QLSQPNLK QVSFGAKGN GITYANMMSIKKE LEAAEVKGIDF KVAEVFH KYLDMEESYVRE QLSQPNLK QVSFGAKGN GITYANMMSIKKE LEAEVKGIDF	180
Sbjct	121	KVAEVFH KYLDMEESYVRE QLSQPNLK QVSFGAKGN GITYANMMSIKKE LEAEVKGIDF	180
Query	181	TTSPNR SYPNGQF ASSFIGLAQ LHENEDGSKS LLG TSGM ESSL NSI LAGTD GI ITYEKDR TTSPNR SYPNGQF ASSFIGLAQ LHENEDGSKS LLG TSGM ESSL NSI LAGD GI ITYEKDR	240
Sbjct	181	TTSPNR SYPNGQF ASSFIGLAQ LHENEDGSKS LLG TSGM ESSL NSI LAGKD GI ITYEKDR	240
Query	241	LGNIVPGTEQV S QRTMDG KDVYTTI S SPLQ SFM ETQMDA FQEVKVGK YM TATL VS A KTG E LGNIVPGTEQV S Q+T+DG KDVYTTI S LQSF M ETQMDA F EKVVGK YM TATL VS A KTG E	300
Sbjct	241	LGNIVPGTEQV S QQTVDG KDVYTTI S STLQSF M ETQMDA FLEKVVGK YM TATL VS A KTG E	300
Query	301	ILATTQRPTFDADTKEGITEDFVWRDILYQSNYEPG STM KVM M LAAAIDNNTFP GG EVFN ILATTQRPTF+ADTKEGITEDFVWRDILYQSNYEPGS MKVM LA++IDNNTFP GE FN	360
Sbjct	301	ILATTQRPTFNADTKEGITEDFVWRDILYQSNYEPGS AMK VMT LASS IDNNTFP SGEYFN	360
Query	361	SSELKIADATIRDWDVNNEGLTGGRMMTFSQGFAHSSNVGM TLLEQKMGDATWLDYLNRFK SSE KIADAT RDWDVN+GLT G MMTF QGFAHSSNVG +LLEQKMGDATWLDYL+R FK	420
Sbjct	361	SSEFKIADATTRDWDVNNDGLT TGGM MTF LQGFAHSSNVGMSLLEQKMGDATWLDYL SR FK	420
Query	421	FGVPTRFGLTDEYAGQLP ADNIVNIAQSSFGQG ISVTQTQMIRAF TAI ANDGVML EPKFI FGVPTRFGLTDEYAGQLP ADNIV +IAQSSFGQG ISVTQTQM+RAFTAI ANDGVML EPKFI	480
Sbjct	421	FGVPTRFGLTDEYAGQLP ADNIVSIAQSSFGQG ISVTQTQMRLRAFTAI ANDGVML EPKFI	480
Query	481	SAIYDPNDQTARKS QKE I VGNPVS KDAASLRT NMVL VGTDPV YGTM NHSTG KPTV TVP SAIYD N+Q+ RKS QKE I VGNPVS K+AAS TR +M+LV GTDP+Y GTM NH TGKP +TVP	540
Sbjct	481	SAIYDTNNQSGRK S QKE I VGNPVS KEAAS TR NHM ILVG TDPL YGTM NH YTG KPIITV P	540
Query	541	GQNVAL KSGTAQ IADEKNGGYLVGLTDYIFSAVSM SPAENPDF ILYVTVQ QPEHSGIQL GQNVA+KSGTAQ IADEKNGGYLVG T+YIFS V+M+PAENPDF ILYVTVQ QPEH+SGIQL	600
Sbjct	541	GQNVAVKSGTAQ IADEKNGGYLVG STNY IF SVT VMN PAENPDF ILYVTVQ QPEH FSGIQL	600
Query	601	GEFANPILERASAMKDSLNLQTTAKALEQV SQQSPYPMPSVKD ISPGD LAEELRRN L VQP GEFA PILERASAMK+SLNLQ+ AK L++V+ +S Y MPS+KDISPG+LAE LRRN+VQP	660
Sbjct	601	GEFATPILERASAMKESLN LQSPAKNLDKV TESSYAMPSIKDISPGELAEALRRNIV QP	660
Query	661	IVVGTGTKIKNSSAEEGKNLAPNQQLILSDKAEEV PDMYGW T KETAETLA KWLNIELEF IVVGTGTKIK +S EEG NLAPNQQL+LSDK EE+PDMYGW KETAET AKWL+IELEF	720
Sbjct	661	IVVGTGTKIKETSVEEGTNLAPNQQLLSDKV EEI PDMYGW KETAETFAKWL DIELEF	720

Query 721 QGSGSTVQKQDVRANTAIKDIKKITLTLGD 750
 +GSGS VQKQDVR NTAIK+IKKI LTLGD
 Sbjct 721 EGSGSVVQKQDVRNTAIKNIKKIKLTLGD 750

>gb|AAL77081.1|AF468152_1 penicillin-binding protein 2X [Streptococcus pneumoniae]
 Length=750

Score = 1307 bits (3382), Expect = 0.0, Method: Composition-based stats.
 Identities = 667/750 (88%), Positives = 711/750 (94%), Gaps = 0/750 (0%)

Query 1	MKWTKR VIRYAT KNRK SPAEN RRRVGKSLSLLSVFVFAI F L VNFAVI I GTGTRG TD LAK	60
Sbjct 1	MKWTKR+ R+A +NRKSPAENR+ VKG +SLL+V +FA+FLVNFAVIIG+G++FGTDL K	
Query 61	EAKKVHQ TTT RVPAKRG TI YDRNGVPIAEDATSYN VYAVIDEN YKSATG KIL YVEKTQFN	120
Sbjct 61	EAKKVHQ TTT RVPAKRG TI YDRNGVPIAEDATSYN VYAVIDEN YKSATG KIL YVEKTQFN	120
Query 121	KVAEV FH KYLDMEES YVREQLSQPNLKQVSFGAKGN GITYANMMSIKKELEAAEVKGIDF	180
Sbjct 121	KVAEV FH KYLDMEES YVREQLSQPNLKQVSFGAKGN GITYANMMSIKKELEAAEVKGIDF	180
Query 181	TTSPNRSYPNGQFASSFIGLAQLHENE DGSKSLLGTSGMESSLNSILAG DGIITYEKDR	240
Sbjct 181	TTSPNRSYPNGQFASSFIGLAQLHENE DGSKSLLGTSGMESSLNSILAG DGIITYEKDR	240
Query 241	LGNIVPGTEQVSQRTMDGKD VYTTI SSPLQS FMETQM DA FQE KVKG KYMTATL VS AKTGE	300
Sbjct 241	LGNIVPGTEQVSQRTMDGKD VYTTI SSPLQS FMETQM DA FQE KVKG KYMTATL VS AKTGE	300
Query 301	I LATTQRPTFDADTKEG ITED FVWRD ILYQSN YEPGSTM KVMMLAAAIDDNNTFP GGEVFN	360
Sbjct 301	I LATTQRPTFDADTKEG+T+DFVWRD ILYQSN YEPGSTM KVM LAAAIDDNNTFP GGEVFN	360
Query 361	SSELKIADATI RDWDVNEGLTGGRMMTF SQGFAHSSNVGM TLLEQKMG DATWLDYLNR FK	420
Sbjct 361	SSELKIADATI RDWDVNEGLTGGRMMTF SQGFAHSSNVGM TLLEQKMG DATWLDYLNR FK	420
Query 421	FGVPTRFGLTDEYAGQLP ADNIVNIAQSSFGQG I SVTQTQ MIR AFTAI ANDGVML EPKFI	480
Sbjct 421	FGVPTRFGLTDEYAGQLP ADNIVNIAQSSFGQG I SVTQTQ MIR AFTAI ANDGVML EPKFI	480
Query 481	SAIYDPNDQTARKS QKEI VGNP VSKDAASL TRTNMVLVGTDPVY GTMYNH STGKPTV TVP	540
Sbjct 481	SAIYDTNNQSVRK S QKEI VGNP VSKDAASL TRTNMVLVGTDPVY GTMYNH STGKPTV TVP	540
Query 541	GQNVALKSGTAQIA DEKNGGYLV GLTDYI FSAV S MS PAEN P D F ILYVTVQQPEHYSGIQL	600
Sbjct 541	GQNVALKSGTAQIA DEKNGGYLV G T+YIFS V+M+PAEN P D F ILYVTVQQPEHYSGIQL	600
Query 601	GEFANPILERASAMKDSLNLQTTAKALEQV SQQSPY PMPSV KDISPGD LAEELRRN L VQP	660
Sbjct 601	GEFANPILERASAMKDSLNLQTTAKALEQV SQQSPY PMPSV KDISPGD LAEELRRN L VQP	660
Query 661	IVVGTGT KIKNSSAEEGKNLAPNQQL L ILSDKAEE VPDMY GWTKETAETLAKWL NIELE F	720
Sbjct 661	IVVGTGT KIKNSSAEEGKNLAPNQQL L ILSDKAEE VPDMY GWTK TAE +KWL NIEL F	720
Query 721	QGSGSTVQKQDVRANTAIKDIKKITLTLGD 750 +GSGS VQKQDVR NTAIK+IKKI LTLGD	
Sbjct 721	EGSGSVVQKQDVRNTAIKNIKKIKLTLGD 750	

>dbj|BAD00939.1| penicillin-binding protein 2X [Streptococcus pneumoniae]
 Length=750

Score = 1307 bits (3382), Expect = 0.0, Method: Composition-based stats.
 Identities = 670/750 (89%), Positives = 711/750 (94%), Gaps = 0/750 (0%)

Query 1	MKWTKR VIRYAT KNRK SPAEN RRRVGKSLSLLSVFVFAI F L VNFAVI I GTGTRG TD LAK	60
Sbjct 1	MKWTK+VIRYAT KNRK SPAEN RRRVGKSLSLLSVFVFAI F L VNFAVI I GTGTRG TD LAK	60
Query 61	EAKKVHQ TTT RVPAKRG TI YDRNGVPIAEDATSYN VYAVIDEN YKSATG KIL YVEKTQFN	120
Sbjct 61	EAKKVHQ TTT RVPAKRG TI YDRNGVPIAEDATSYN VYAVIDEN YKSATG KIL YVEKTQFN	120
Query 121	KVAEV FH KYLDMEES YVREQLSQPNLKQVSFGAKGN GITYANMMSIKKELEAAEVKGIDF	180
Sbjct 121	KVAEV FH KYLDMEES YVREQLSQPNLKQVSFGAKGN GITYANMMSIKKELEAAEVKGIDF	180
Query 181	TTSPNRSYPNGQFASSFIGLAQLHENE DGSKSLLGTSGMESSLNSILAG DGIITYEKDR	240
Sbjct 181	TTSPNRSYPNGQFASSFIGLAQLHENE DGSKSLLGTSGMESSLNSILAG DGIITYEKDR	240

Query	241	LGNIVPGTEQVSQRTMDGKDVTIISPLQSFMETQMDAFQEKVKGKYMTATLVSAKTGE +GNIVPGTE VSQ+T+DGKDVTI+SSPLQSFMETQMDAF +KVKGKYMTATLVSAKTGE	300
Sbjct	241	VGNIVPGTELVSQQTVGDKDVTIISPLQSFMETQMDAFLQKVKGKYMTATLVSAKTGE	300
Query	301	ILATTQRPTFDADTKEGITEDFVWRDILYQSNYEPGSTMVKVMMALAAIDNNNTFPGEVFN ILATTQRPTF+ADTKEGITEDFVWRDILYQSNYEPGS KVMMMA++IDNNNTFP GE FN	360
Sbjct	301	ILATTQRPTFNADTKEGITEDFVWRDILYQSNYEPGSASFVKVMMALASSIDNNNTFPSGEYFN	360
Query	361	SSELKIADATIRDWDVNNEGLTGRMMTFSQGFAHSSNVGMTLLEQKMGDATWLDYLNRFK SSE KIADAT RDWDVNNEGLT G MMTF QGFAHSSNVG +LLEQKMGDATWLDYL RFK	420
Sbjct	361	SSEFKIADATTRDWDVNNEGLTGGMMTFLQGFAHSSNVGTSLLLEQKMGDATWLDYLKRFK	420
Query	421	FGVPTRFGLTDEYAGQLPADNIVNIAQSSFGQGISVTQTQMIRAFTAIANDGVMLEPKFI FGVPTRFGLTDEYAGQLPADNIV+IAQSSFGQGISVTQTQM+RAFTAIAANDGVMLEPKFI	480
Sbjct	421	FGVPTRFGLTDEYAGQLPADNIVSIAQSSFGQGISVTQTQMLRAFTAIANDGVMLEPKFI	480
Query	481	SAIYDPNDQTARKSQKEIVGNPVSKDAASLTRTNMVLVGTDPVYGTMYNHSTGKPTVTVP SAIYD N+Q+ RKSQKEIVGNPVS+ AAS TR +M+LVGTD+YGTMYNH TGKP +TVP	540
Sbjct	481	SAIYDTNNQSVRKSQKEIVGNPVSKEAASTTRNHMILVGTDPYGTMYNHYTGKPIITV	540
Query	541	GQNVALKSGTAQIADEKNGGYLVGLTDYIFSAVSMSPAENPDFILYVTVQQPEHYSGIQL GQNV+A KSGTAQIADEKNGGYLVG T+YIFS V+M+PAENPDFILYVTVQQPEHYSGIQL	600
Sbjct	541	GQNVAVKSGTAQIADEKNGGYLVGSTNYIFSVVTMNP+ AENPDFILYVTVQQPEHYSGIQL	600
Query	601	GEFANPILERASAMKDSLNLQTTAKALEQVSQSPYPMPSVKDISPGDLAEELRRNLVQP GEFA PILERASAMK+SLNLQ+ AK L++V+ +S Y MPS+KDISPG+LAE LRRN+VQP	660
Sbjct	601	GEFATPILERASAMKESLNQSPAKNLKVTESSYAMPSIKDISPGELAEALRRNIVQP	660
Query	661	IVVGTGKIKKNSSAEEGKNLAPNQQVLILSDKAEEVPDMYGWTKETAETLAKWLNIELEF IVVGTGKIK +S EEG NLAPNQQVL+LSDK EE+PDHYGW KETAET AKWL+IELEF	720
Sbjct	661	IVVGTGKIKETSVEEGTNLAPNQQVLLSDKVEEIPDMYGWKKETAETFAKWL DIELEF	720
Query	721	QGSGSTVQKQDVRANTAIAKDIKKITLTLD 750 +GSGS VQKQDVR NTAIK+IKKI LTLD	750
Sbjct	721	EGSGSVVQKQDVRTNTAIKNIKKIKLTLD 750	750

>dbj|BAD00935.1| penicillin-binding protein 2X [Streptococcus pneumoniae]
Length=750

Score = 1306 bits (3380), Expect = 0.0, Method: Composition-based stats.
Identities = 667/750 (88%), Positives = 715/750 (95%), Gaps = 0/750 (0%)

Query	1	MKWTKRVIRYATKNRKSPAENRRRVGKSLSSLGVFAI FLVNFAVIIGTGTRFGTDLAK MKWTKRVIRYATKNRKSPAENRRRVGKSLSSLGVFA+FLVNFAVIIGTGTRFGTDLAK	60
Sbjct	1	MKWTKRVIRYATKNRKSPAENRRRVGKSLSSLGVFAVFLVNFAVIIGTGTRFGTDLAK	60
Query	61	EAKKVKHQTTRVPAKRGTIYDRNGVPIAEDATSYNVYAVIDENYKSATGKILYVEKTQFN EAKKVKHQTTRVPAKRGTIYDRNGVPIAEDATSYNVYAVIDENYKSATGKILYVEKTQFN	120
Sbjct	61	EAKKVKHQTTRVPAKRGTIYDRNGVPIAEDATSYNVYAVIDENYKSATGKILYVEKTQFN	120
Query	121	KVAEVFHKYLDMEESYVREQLSQPNLKQVSFGAKGNIGINIANMMSIKKELEAAEVKGIDF KVAEVFHKYLDMEESYVREQLSQPNLKQVSFG+KGNIGINIANMMSIKK+LE A+V+GIDF	180
Sbjct	121	KVAEVFHKYLDMEESYVREQLSQPNLKQVSFGSKGNIGINIANMMSIKKDLETAKVEGIDF	180
Query	181	TTSPNRSYPNGQFASSFIGLAQLHENEDGSKSLLGTSMESSLNSILAGTDGIITYEKDR TTSPNRSYPNG+FASSFIGLAQLHENEDGSKSL+GTSG+ESSLNS+LAGTDGIITYEKDR	240
Sbjct	181	TTSPNRSYPNGKFASSFIGLAQLHENEDGSKSLIGTSGVESSLNSLLAGTDGIITYEKDR	240
Query	241	LGNIVPGTEQVSQRTMDGKDVTIISPLQSFMETQMDAFQEKVKGKYMTATLVSAKTGE LGNIVPGTEQV++T+ +GKDVTI+SSPLQSFME+QMDAFQE+KGKYMTATLVSAKTGE	300
Sbjct	241	LGNIVPGTEQVTRQTVNGKDVTIISPLQSFMESQMDAFQEKLKGKYMTATLVSAKTGE	300
Query	301	ILATTQRPTFDADTKEGITEDFVWRDILYQSNYEPGSTMVKVMMALAAIDNNNTFPGEVFN ILATTQRPTFDADTKEGITEDFVWRDILYQSNYEPGS MKVM LA++IDNNNTFP GE FN	360
Sbjct	301	ILATTQRPTFDADTKEGITEDFVWRDILYQSNYEPGSAMKVMTLASSIDNNNTFPSGEYFN	360
Query	361	SSELKIADATIRDWDVNNEGLTGRMMTFSQGFAHSSNVGMTLLEQKMGDATWLDYLNRFK SSE KIADAT RDWDVNNEGLT G MMTF QGFAHSSNVG +LLEQKMGDATWLDYL RFK	420
Sbjct	361	SSEFKIADATTRDWDVNNEGLTGGMMTFLQGFAHSSNVGMSLLEQKMGDATWLDYLKRFK	420
Query	421	FGVPTRFGLTDEYAGQLPADNIVNIAQSSFGQGISVTQTQMIRAFTAIANDGVMLEPKFI FGVPTRFGLTDEYAGQLPADNIV+IAQSSFGQGISVTQTQM+RAFTAIAANDGVMLEPKFI	480
Sbjct	421	FGVPTRFGLTDEYAGQLPADNIVSIAQSSFGQGISVTQTQMLRAFTAIANDGVMLEPKFI	480
Query	481	SAIYDPNDQTARKSQKEIVGNPVSKDAASLTRTNMVLVGTDPVYGTMYNHSTGKPTVTVP SAIYD N+Q+ RKSQKEIVGNPVS+ AAS TR +M+LVGTD+YGTMYNH TGKP +TVP	540
Sbjct	481	SAIYDTNNQSVRKSQKEIVGNPVSKEAASTTRNHMILVGTDPYGTMYNHYTGKPIITV	540
Query	541	GQNVALKSGTAQIADEKNGGYLVGLTDYIFSAVSMSPAENPDFILYVTVQQPEHYSGIQL GQNV+A KSGTAQIADEKNGGYLVG T+YIFS V+M+PAENPDFILYVTVQQPEHYSGIQL	600
Sbjct	541	GQNVAVKSGTAQIADEKNGGYLVGSTNYIFSVVTMNP+ AENPDFILYVTVQQPEHYSGIQL	600
Query	601	GEFANPILERASAMKDSLNLQTTAKALEQVSQSPYPMPSVKDISPGDLAEELRRNLVQP GEFA PILERASAMK+SLNLQ+ AK L++V+ +S Y MPS+KDISPG+LAE LRRN+VQP	660
Sbjct	601	GEFATPILERASAMKESLNQSPAKNLKVTESSYAMPSIKDISPGELAEALRRNIVQP	660

• Query	661	IVVGTGKIKNSSAEEGKNLAPNQQVLILSDKAEEVPDMYGWTKETAETLAKWLNLIELEF	720
Sbjct	661	IVVGTGKIK +S EEG NLAPNQQVL+LSDK EE+PDGYW KETAET AKWL+IELEF	720
- Query	721	QGSGSTVQKQDVRANTAIKDIKKITLTG 750	
Sbjct	721	+GSGS VQKQDVR NTAIK+IKKI LTLG 750	
>dbj BAD00906.1 penicillin-binding protein 2X [Streptococcus pneumoniae]			
Length=750			
Score = 1305 bits (3378), Expect = 0.0, Method: Composition-based stats.			
Identities = 669/750 (89%), Positives = 710/750 (94%), Gaps = 0/750 (0%)			
Query	1	MKWTKRVIYATKNRSPAENRRVGKSLSSLGVFAIFLVNFAVIIGTGTRGTDLAK	60
Sbjct	1	MKWTK+VIRYATKNRSPAENRRVGKSLSSLGVFA+FLVNFAVIIGTGTRGTDLAK	60
Query	61	EAKKVHQTRTVPAKRGTIYDRNGVPIAEDATSYNVYAVIDENYSATGKILYVEKTQFN	120
Sbjct	61	EAKKVHQTRTVPAKRGTIYDRNGVPIAEDATSYNVYAVID+ YKSATGKILYVE QFN	120
Query	121	KVAEVFHKLDMEESYVREQLSQPNLKQVSFGAKGNIGITYANMMSIKKELEAAEVKGIDF	180
Sbjct	121	KVAEVFHKLDMEESYVREQLSQPNLKQVSFG+KGNIGITYANMM+IKKELE AEVKGIDF	180
Query	181	TTSPNRSPNGQFASSFIGLAQLHENEDGSKSLLGTSGMESLNSILAGTDGIITYEKDR	240
Sbjct	181	TTSPNRSPNGQFASSFIGLAQLHENEDGSKSLLGTSGMESLN ILAGTDGIITYEKDR	240
Query	241	LGNIVPGTEQVSQRTMDGKDVTIISPLQSFMETQMDAFQEKVKGKYMTATLVSAKTGE	300
Sbjct	241	LGNIVPGTEQVSQ+T+DGKDVTI+SSPLQSFMETQMDAF EKVVKGKYMTATLVSAKTGE	300
Query	301	ILATTQRPTFDADTKEGITEDFVWRDILYQSNYEPGSTMVKVMLAAAIDNNNTFPGEVFN	360
Sbjct	301	ILATTQRPTF+ADTKEGITEDFVWRDILYQSNYEPGS MKVM LA+IDNNNTFP GE FN	360
Query	361	SSELKIADATIRDWDVNEGLTGGRMMTFSQGFAHSSNVGMTLLEQKMGDATWLDYLNRFK	420
Sbjct	361	SSE KIADAT RDWDVN+GLT G MMFT QGFAHSSNVGM+LLEQKMGDATWLDYL R FK	420
Query	421	FGVPTRFGLTDEYAGQLPADNIVNIAQSSFGQGISVTOTQMIRFTAIAANDGVMLEPKFI	480
Sbjct	421	FGVPTRFGLTDEYAGQLPADNIV+IAQSSFGQGISVTOTQM+RAFTAIAANDGVMLEPKFI	480
Query	481	SAIYDPNDQTARKSQKEIVGNPVSCKDAASLRTTNMVLVGTDPVYGTMYNHSTGKPTVTVP	540
Sbjct	481	SAIYD N+Q+ RKSQKEIVGNPVSCK+AAS TR +M+LVGTD+YGTMYNH TGKP +TVP	540
Query	541	SAIYDTNNQSVRKSQKEIVGNPVSKEAASTRNHMILVGTDPYGTMYNHGTGKPIITVP	540
Sbjct	541	SAIYDTNNQSVRKSQKEIVGNPVSKEAASTRNHMILVGTDPYGTMYNHGTGKPIITVP	540
Query	601	GQNVALKSGTAQIADEKNGGYLVGLTDYIFSAVSMSPAENPDFILYVTVQQPEHYSGIQL	600
Sbjct	601	GQNVA+KSGTAQIADEKNGGYLVG T+YIFS V+M+PAENPDFILYVTVQQPEHYSGIQL	600
Query	661	GQNVALKSGTAQIADEKNGGYLVGSTNYIFSVVTMNPNAENPDFILYVTVQQPEHYSGIQL	600
Sbjct	661	GQNVALKSGTAQIADEKNGGYLVGSTNYIFSVVTMNPNAENPDFILYVTVQQPEHYSGIQL	600
Query	661	GEFANPILEASAMKDSLNLQTTAKALEQVSQQSPYPPMSVKDISPGDLAELRRNLVQP	660
Sbjct	661	GEFA PILEASAMK+SLNLQ+ AK L++V+ +S Y MPS+KDISPG+LAE LRRN+VQP	660
Query	661	GEFATPILEASAMKESLNQSPAKNLDKVTESSYAMPSIKDISPGELAEALRRNIVQP	660
Sbjct	661	GEFATPILEASAMKESLNQSPAKNLDKVTESSYAMPSIKDISPGELAEALRRNIVQP	660
Query	721	IVVGTGKIKNSSAEEGKNLAPNQQVLILSDKAEEVPDMYGWTKETAETLAKWLNLIELEF	720
Sbjct	721	IVVGTGKIK +S EEG NLAPNQQVL+LSDK EE+PDGYW KETAET AKWL+IELEF	720
Query	721	QGSGSTVQKQDVRANTAIKDIKKITLTG 750	
Sbjct	721	+GSGS VQKQDVR NTAIK+IKKI LTLG 750	

>dbj|BAD00937.1| penicillin-binding protein 2X [Streptococcus pneumoniae]

Length=750

Score = 1303 bits (3373), Expect = 0.0, Method: Composition-based stats.
Identities = 664/750 (88%), Positives = 711/750 (94%), Gaps = 0/750 (0%)

Query	1	MKWTKRVIYATKNRSPAENRRVGKSLSSLGVFAIFLVNFAVIIGTGTRGTDLAK	60
Sbjct	1	MKWTKRVIYATKNRSPAENRRVGKSLSSLGVFA+FLVNFAVIIGTGTRGTDLAK	60
Query	61	EAKKVHQTRTVPAKRGTIYDRNGVPIAEDATSYNVYAVIDENYSATGKILYVEKTQFN	120
Sbjct	61	EAKKVHQITRTVPAKRGTIYDRNGVPIAEDATSYNVYAVID+ YKSATGKILYVE QFN	120
Query	121	KVAEVFHKLDMEESYVREQLSQPNLKQVSFGAKGNIGITYANMMSIKKELEAAEVKGIDF	180
Sbjct	121	KVAEVFHKLDM+E+YV+EQL+OPNL QVSFGAKGNIGITYANMM+IKK+L+ A V+GIDF	180

Query	181	TTSPNRSPNGQFASSFIGLAQLHENEDGSKSLLGTSGMESSLNSILAGTDGIITYEKDR	240
Sbjct	181	TTSPNRSPNGQFASSFIGLAQLHENEDGSKSLLGTSG+ESSLN+ILAGTDGIITYEKDR	240
Query	241	LGNIVPGTEQVSQRTMDGKDVTYTTISSLPLQSFMETQMDAFQEKVKGKYMTATLVSAKTGE +GNIVPGTE VSQ+T+DGKDVTYTT+SSPLOSFMETQMDAF EKVKGKYMTATLVSAKTGE	300
Sbjct	241	VGNIVPGTELVSQQTVDGKDVTYTTLSSPLQSFMETQMDAFLEKVKGKYMTATLVSAKTGE	300
Query	301	ILATTQRPTFDADTKEGITEDFVWRDILYQSNSYEPGSTMVKVMMAAAIDNNTFPGGEVFN ILATTQRPTF+ADTKEGITEDFVWRDILYQSNSYEPGS MKVM LA++IDNNTFP GE FN	360
Sbjct	301	ILATTQRPTFNADTKEGITEDFVWRDILYQSNSYEPGSAMVKVMTLASSIDNNTFPSGEYFN	360
Query	361	SSELKIADATIRDWDVNEGLTGGRMMTFSQGFAHSSNVGMTLLEQKMGDATWLDPNRFK SSE KIADAT RDWDVNEGLT G MMTF QGFAHSSNVGM+LLEQKMGDATWLDPNRFK	420
Sbjct	361	SSEFKIADATTRDWDVNEGLTGGMFTFLQGFAHSSNVGMSLLEQKMGDATWLDPNRFK	420
Query	421	FGVPTRFGLTDEYAGQLPADNIVNIAQSSFGQGISVTQTQMIRRAFTAIANDGVMLEPKFI FGVPTRFGLTDEYAGQLPADNIV+IAQSSFGQGISVTQTQM+RAFTAIANDGVMLEPKFI	480
Sbjct	421	FGVPTRFGLTDEYAGQLPADNIVSIAQSSFGQGISVTQTQMLRAFTAIANDGVMLEPKFI	480
Query	481	SAIYDPNDOTARKSQKEIVGNPVSCKDAASLRTNMVLVGTDPVYGTMYNHSTGKPTVTVP SAIYD N+Q+ RKSQKEIVGNPVSCK+AAS TR +M+LVGTD+YGTMYNH TGKP +TVP	540
Sbjct	481	SAIYDTNNQSVRKSQKEIVGNPVSCKAASSTRRNHMILVGTDPYGTMYNHSTGKPTVTVP	540
Query	541	GQNVALKSGTAQIADEKNGGYLVGLTDYIFSAVMSSPAENPDFILYVTVQQPEHYSGIQL GQNVA+KSGTAQIADEKNGGYLVG T+YIFSAV+M+PAENPDFILYVTVQQPEHYSGIQL	600
Sbjct	541	GQNVAVKSGTAQIADEKNGGYLVGSTNYIFSAVTMNPAAENPDFILYVTVQQPEHYSGIQL	600
Query	601	GEFANPILERASAMKDSLNLQTTAKALEQVSQQSPYPMPSVKDISPGDLAEELRRNLVQP GEF PIILERASAMK+SLNLQ+ AK L++V+ +S Y MPS+KDISPGDLAEELRRN+VQP	660
Sbjct	601	GEFVTPILERASAMKESLNQSPAKNLKDVTTESSYAMPSIKDISPGDLAEELRRNIVQP	660
Query	661	IVVGTTGKIKNNSAEEGKNLAPNQQVLILSDKAEEVPDMYGWTKETAETLAKWLNIELEF IV+G GTKIKN+S EEGKNLAPNQQVL+LSDK EE+PDMDYWTK TAE +KWLNLIELEF	720
Sbjct	661	IVIGAGTKIKNNSAEEGKNLAPNQQVLLSDKVEEIPDMYWTKTTAEAFSKWLNLIELEF	720
Query	721	QGSGSTVQKQDVRANTAIKDIKKITLTLDG 750 +GSGSTVQKQDVRANTAIKDIKKITLTLDG	750
Sbjct	721	EGSGSTVQKQDVRANTAIKDIKKITLTLDG 750	750

> pdb|1RP5|A S Chain A, Pbp2x From Streptococcus Pneumoniae Strain 5259 With Reduced Susceptibility To Beta-Lactam Antibiotics

pdb|1RP5|B S Chain B, Pbp2x From Streptococcus Pneumoniae Strain 5259 With Reduced Susceptibility To Beta-Lactam Antibiotics

emb|CAE53270.1| penicillin-binding protein 2x [Streptococcus pneumoniae] Length=702

Score = 1297 bits (3357), Expect = 0.0, Method: Composition-based stats.
Identities = 674/702 (96%), Positives = 688/702 (98%), Gaps = 0/702 (0%)

Query	49	GTGTRFGTDLAKEAKKVHQTTRTVPAKRGTIYDRNGVPIAEDATSYNVYAVIDENYKSAT GTGTRFGTDLAKEAKKVHQTTRTVPAKRGTIYDRNGVPIAEDATSYNVYAVIDENYKSAT	108
Sbjct	1	GTGTRFGTDLAKEAKKVHQTTRTVPAKRGTIYDRNGVPIAEDATSYNVYAVIDENYKSAT	60
Query	109	GKILYVEKTQFNKVAEVFKYLDMEESYVREQLSQPNLKQVSFGAKGNGITYANMMSIKK GKILYVEKTQFNKVAEVFKYLDMEESYVREQLSQPNLKQVSFGAKGNGITYANMMSIKK	168
Sbjct	61	GKILYVEKTQFNKVAEVFKYLDMEESYVREQLSQPNLKQVSFGAKGNGITYANMMSIKK	120
Query	169	ELEAAEVKGIDFTTSPNRSYPNGQFASSFIGLAQLHENEDGSKSLLGTSGMESSLNSILA ELE AEVKGIDFTTSPNRSYPNGQFASSFIGLAQLHENEDGSKSLLGTSGMESSLNSILA	228
Sbjct	121	ELETAEVKGIDFTTSPNRSYPNGQFASSFIGLAQLHENEDGSKSLLGTSGMESSLNSILA	180
Query	229	GTDGIITYEKDRLGNIVPGTEQVSQRTMDGKDVTYTTISSLPLQSFMETQMDAFQEKVKGKY GTDGIITYEKDRLGNIVPGTEQVSQ+T+DGKDVTYTTISSLPLQSFMETQMDAFQEKVKGKY	288
Sbjct	181	GTDGIITYEKDRLGNIVPGTEQVSQQTVDGKDVTYTTISSLPLQSFMETQMDAFQEKVKGKY	240
Query	289	MTATLVSAKTGEILATTQRPTFDADTKEGITEDFVWRDILYQSNSYEPGSTMVKVMMAAA MTATLVSAKTGEILATTQRPTFDADTKEGITEDFVWRDILYQSNSYEPGSTMVKVMMAAA	348
Sbjct	241	MTATLVSAKTGEILATTQRPTFDADTKEGITEDFVWRDILYQSNSYEPGSTMVKVMMAAA	300
Query	349	DNNTFPGGEVFNSSELKIADATIRDWDVNEGLTGGRMMTFSQGFAHSSNVGMTLLEQKMG DNNTFPGGEVFNSSELKIADATIRDWDVNEGLTGGRMMTFSQGFAHSSNVGMTLLEQKMG	408
Sbjct	301	DNNTFPGGEVFNSSELKIADATIRDWDVNEGLTGGRMMTFSQGFAHSSNVGMTLLEQKMG	360
Query	409	DATWLDYLNRFKFGVPTRFGLTDEYAGQLPADNIVNIAQSSFGQGISVTQTQMIRRAFTAI DATWLDYLNRFKFGVPTRFGLTDEYAGQLPADNIVNIA S+FGQGISVTQTQM+RAFTAI	468
Sbjct	361	DATWLDYLNRFKFGVPTRFGLTDEYAGQLPADNIVNIA S+FGQGISVTQTQM+RAFTAI	420
Query	469	ANDGVMLEPKFISAIYDPNDOTARKSQKEIVGNPVSCKDAASLRTNMVLVGTDPVYGTMY ANDGVMLEPKFISA+YDPNDQ+ RKSQKEIVGNPVSCK+AAS+TR +MV+VGTDP YGTMY	528
Sbjct	421	ANDGVMLEPKFISALYDPNDQSVRKSQKEIVGNPVSCKAASVTRDHMVMVGTDPYGTMY	480

NCBI Blast: PBP2X-R6

Query	529	NHSTGKPTVTVPQONVALKSGTAQIADEKNGGYLVGLTDYIFSAVSMSPAENPDFILYVT	588
Sbjct	481	NHSTGKATVNVPQONVALKSGTA+IADEKNGGYL G T+ IFS VSM PAENPDFILYVT	540
Query	589	VQQPEHYSGIQLGEFANPILERASAMKDSLNLQTTAKALEQVSQQSPYPMPSVKDISPGD	648
Sbjct	541	VQQPEHYSGIQLGEFANPILERASAMK+SLNLQTTAKALEQVSQQSPYPMPSVKDISPGD	600
Query	649	LAEELRRNVLQPIIVVGTVGT KIKNSSAEEGKNLAPNQQLILSDKAEEVPDMYGWTKETAE	708
Sbjct	601	LAEELRRNVLQPIIVVGTVGT KIKNSSAEEGKNLAPNQQLILSDKAEEVPDMYGWTKETAE	660
Query	709	T LAKWL NIELE F QGS G S T V Q K Q D V R V A N T A I K D I K K I T L T G D	750
Sbjct	661	T AKWL NIELE F + G S G S T V Q K Q D V R V A N T A I K D I K K I K L T L G D	702

>dbj|BAD00914.1| penicillin-binding protein 2X [Streptococcus pneumoniae]
 dbj|BAD00930.1| penicillin-binding protein 2X [Streptococcus pneumoniae]
 dbj|BAD00931.1| penicillin-binding protein 2X [Streptococcus pneumoniae]
 dbj|BAD00933.1| penicillin-binding protein 2X [Streptococcus pneumoniae]

Length=750

Score = 1296 bits (3354), Expect = 0.0, Method: Composition-based stats.
 Identities = 662/750 (88%), Positives = 707/750 (94%), Gaps = 0/750 (0%)

Query	1	MWTKR VIR YAT KNR SPA ENR R V G K S L S L S V F V F A I F L V N F A V I I G T G T R F G T D L A K	60
Sbjct	1	MWTKR VIR YAT KNR SPA ENR R V G K S L S L S V F V F A + F L V N F A V I I G + G ++ F G T D L K	60
Query	61	EAKK V H Q T T R T V P A K R G T I Y D R N G V P I A E D A T S Y N V Y A V I D E N Y K S A T G K I L Y V E K T Q F N	120
Sbjct	61	EAKK V H Q T T R T V P A K R G T I Y D R N G V P I A E D A T S Y N V Y A V I D + Y K S A T G K I L Y V E Q F N	120
Query	121	KVAE V F H K Y L D M E E S Y V R E Q L S Q P N L K Q V S F G A K G N G I T Y A N M M S I K K E L E A A E V K G I D F	180
Sbjct	121	KVAE V F H K Y L D M + E + Y V + E Q L S Q P N L Q V S F G A K G N G I T Y A N M M + I K K E L E A E V K G I D F	180
Query	181	T T S P N R S Y P N G Q F A S S F I G L A Q L H E N E D G S K S L L G T S G M E S S L N S I L A G T D G I I T Y E K D R	240
Sbjct	181	T T S P N R S Y P N G Q F A S S F I G L A Q L H E N E D G S K S L L G T S G M E S S L N S I L A G K D G I I T Y E K D R	240
Query	241	L G N I V P G T E Q V S Q R T M D G K D V Y T T I S S P L Q S F M E T Q M D A F Q E K V K G K Y M T A T L V S A K T G E	300
Sbjct	241	L G N I V P G T E Q V S Q + T + D G K D V Y T T + S S P L Q S F M E T Q M D A F E K V K G K Y M T A T L V S A K T G E	300
Query	301	I L A T T Q R P T F D A D T K E G I T E D F V W R D I L Y Q S N Y E P G S T M K V M M L A A A I D N N T F P G G E V F N	360
Sbjct	301	I L A T T Q R P T F + A D T K E G I T E D F V W R D I L Y Q S N Y E P G S M K V M L A + + I D N N T F P G E F N	360
Query	361	S S E L K I A D A T I R D W D V N E G L T G G R M M T F S O Q F A H S S N V G M T L L E Q K M G D A T W L D Y L N R F K	420
Sbjct	361	S S E F K I A D A T T R D W D V N D G L T T G G M M T F L Q G F A H S S N V G M S L L E Q K M G D A T W L D Y L K R F K	420
Query	421	F G V P T R F G L T D E Y A G Q L P A D N I V N I A Q S S F G Q G I S V T Q T Q M I R A F T A I A N D G V M L E P K F I	480
Sbjct	421	F G V P T R F G L T D E Y A G Q L P A D N I V + I A Q S S F G Q G I S V T Q T Q M + R A F T A I A N D G V M L E P K F I	480
Query	481	S A I Y D P N D Q T A R K S Q K E I V G N P V S K D A A S L T R T N M V L V G T D P V Y G T M Y N H S T G K P T V T V P	540
Sbjct	481	S A I Y D N + Q + R K S Q K E I V G N P V S K + A A S T R + M + L V G T D P + Y G T M Y N H T G K P + T V P	540
Query	541	G Q N V A L K S G T A Q I A D E K N G G Y L V G L T D Y I F S A V S M S P A E N P D F I L Y V T V Q Q P E H Y S G I Q L	600
Sbjct	541	G Q N V A V K S G T A Q I A D E K N G G Y L V G S T N Y I F S V V T M N P A E N P D F I L Y V T V Q Q P E H Y S G I Q L	600
Query	601	G E F A N P I L E R A S A M K D S L N L Q T T A K A L E Q V S Q Q S P Y P M P S V K D I S P G D L A E E L R R N L V Q P	660
Sbjct	601	G E F A P I L E R A S A M K + S L N L Q + A K L + + V + + S Y M P S + K D I S P G + L A E L R R N + V Q P	660
Query	661	I V V G T G T K I K N S S A E E G K N L A P N Q Q V L I L S D K A E E V P D M Y G W T K E A T E T L A K W L N I E L E F	720
Sbjct	661	I V V G T G T K I K + S E E G N L A P N Q Q V L + L S D K E E + P D M Y G W K E A T E T A K W L + I E L E F	720
Query	721	Q G S G S T V Q K Q D V R V A N T A I K D I K K I T L T G D	750
Sbjct	721	+ G S G S V Q K Q D V R T N T A I K N I K K I K L T L G D	750

>dbj|BAD00928.1| penicillin-binding protein 2X [Streptococcus pneumoniae]
 Length=750

Score = 1294 bits (3348), Expect = 0.0, Method: Composition-based stats.
 Identities = 662/750 (88%), Positives = 706/750 (94%), Gaps = 0/750 (0%)

Query 1 MKWTKR VIR YAT KNR SPA ENR R V G K S L S L S V F V F A I F L V N F A V I I G T G T R F G T D L A K 60

Sbjct	1	MKWTKRVIRYATKNRKP SAENRRVGKSLSLLSVFVFA+FLVNFAVIIG+G++FGTDL K	60
Query	61	EAKKVHQTTRTVPAKRGTIYDRNGVPIAEDATS YNVYAVIDENYSATGKILYVEKTQFN	120
Sbjct	61	EAKKVHQTTRTVPAKRGTIYDRNGVPIAEDATS YNVYAVID+ YKSATGKILYVE QFN	120
Query	121	KVAEVFHKLDMEE SYVREQLSQPNLKQVSFGAKGN GITYANMMSIKKELEAAEVKGIDF	180
Sbjct	121	KVAEVFHKLDM+E+YV+ EQLSQPNL QVSFGAKGN GITYANMM+IKKELE AEVK KGIDF	180
Query	181	TTSPNRSPNGQFASSFIGLAQLH ENEDGSKSLLGTSGMESSLNSI LAGTDGIITYEKDR	240
Sbjct	181	TTSPNRSPNGQFASSFIGLAQLH ENEDGSKSLLGTSGMESSLNSI LAGTDGIITYEKDR	240
Query	241	LGNIVPGTEQVSQRTMDGKD VYTTISPLQSFMETQMDAF QEKFVKGKYM TATLVS AKTGE	300
Sbjct	241	LGNIVPGTEQVSQ+T+DGK DVTYTT+SSPLQSFMETQMDAF EKFVKGKYM TATLVS AKTGE	300
Query	301	ILATTQRPTFDADTK EGITEDFVWRDILYQS NYEPGSTM KVMMLAAA IDNNTFP GE FN	360
Sbjct	301	ILATTQRPTF +ADTK EGITEDFVWRDILYQS NYEPGS AFKV MTLASS IDNNTFPS GEYFN	360
Query	361	SSELKIADATIRDWDV NEGLTGGRM MTFSQG FAHSSNV GMLLEQ KMG DATWLDY LNRFK	420
Sbjct	361	SSE KIADAT RDWDVN GLT G MMTFSQG FAHSSNVG +LLEQ KMG DATWLDY RFK	420
Query	421	FGVPTRFGLTDEYAG QLPADNIV NIAQSSFG QGISV TQTM RAFTAI ANDGV MLEPKFI	480
Sbjct	421	FGVPTRFGLTDEYAG QLPADNIV NIAQSSFG QGISV TQTM RAFTAI ANDGV MLEPKFI	480
Query	481	SAIYDPNDQT ARKS SQKEIV GNP VSK DAAS LRT TNM VLV GTD PVY GT MYH NST GK PT TV P	540
Sbjct	481	SAIYD N+Q+ RKS SQKEIV G P V S+D AAS LRT NM+L V G T D P Y G T M Y H TG K P +T V P	540
Query	541	GQNVALKSGTAQ IADEKNGGY LVGL TDY IFSAV SMS PAEN PDF ILY V TV QQPE H SGIQL	600
Sbjct	541	GQNV A+K SGT A Q IA DE K N G G Y L V G S T N Y I F S V V T M N P A E N P D F I L Y V T V Q Q P E H + SGIQL	600
Query	601	GEFAN PILE RASAM KDSL NLQ TTAK ALE QV SQ SPY PM PSV KD IS PG D LAE EL RR NL V Q P GEFA PILE RASAM K+SL NLQ+ AK L++V+ +S Y MPS+K DIS PG+LAE LRR NL V Q P GEFA PILE RASAM KES SLN LQ SPA K NL DK V T ESS Y AMP SI K DI SP GEL AE AL RR NI V Q P	660
Sbjct	601	GEFA PILE RASAM KES SLN LQ SPA K NL DK V T ESS Y AMP SI K DI SP GEL AE AL RR NI V Q P	660
Query	661	IVVGTG TKIK KNSS AEE GK NL AP NQ QV L I L SD KA EE V P D M Y G W K T A E T A K W L I E L F	720
Sbjct	661	IVVGTG TKIK +S EEG NL AP NQ QV L I L SD KA EE V P D M Y G W K T A E T A K W L I E L F	720
Query	721	QGSG STV QK QD VR R A N T A I K D I K K I L T L G D	750
Sbjct	721	+GSGS VQ QD VR NT AI K D I K K I L T L G D	750

> pdb|1PMD| S Chain , Penicillin-Binding Protein 2x (Pbp-2x)
Length=675

Score = 1294 bits (3348), Expect = 0.0, Method: Composition-based stats.
Identities = 675/675 (100%), Positives = 675/675 (100%), Gaps = 0/675 (0%)

Query	76	RGTIYDRNGVPIAEDATS YNVYAVIDENYSATGKILY VEKTQFNKVAEVFH KYLDMEES	135
Sbjct	1	RGTIYDRNGVPIAEDATS YNVYAVIDENYSATGKILY VEKTQFNKVAEVFH KYLDMEES	60
Query	136	YVREQLSQPNLKQVSFG AKGN GITYAN MMSIK KELEAA EVKG IDFTT SPNRS YPNGQ FAS	195
Sbjct	61	YVREQLSQPNLKQVSFG AKGN GITYAN MMSIK KELEAA EVKG IDFTT SPNRS YPNGQ FAS	120
Query	196	SFIGLAQLH ENEDG SKSLL GTSG MESS LNSI LAGT DGI ITYE KDR LGN I V PG TE Q V S Q R T	255
Sbjct	121	SFIGLAQLH ENEDG SKSLL GTSG MESS LNSI LAGT DGI ITYE KDR LGN I V PG TE Q V S Q R T	180
Query	256	MDGKD VYTT ISPL QSFM ETQMD AFQE KVG KYM TATL VSA KTGE ILAT TQR PTFD ADTK	315
Sbjct	181	MDGKD VYTT ISPL QSFM ETQMD AFQE KVG KYM TATL VSA KTGE ILAT TQR PTFD ADTK	240
Query	316	EGITED FV WRD ILYQS NYEP GSTM KVM MLAAA IDN NTP FPG GEV F NS SEL KI AD AT I RD WD	375
Sbjct	241	EGITED FV WRD ILYQS NYEP GSTM KVM MLAAA IDN NTP FPG GEV F NS SEL KI AD AT I RD WD	300
Query	376	VNEG LTGG GRMM TF SQG FAH SSN VG M T L LEQ K MG D AT W LD Y LN R F G V P T R F G L T D E Y A G	435
Sbjct	301	VNEG LTGG GRMM TF SQG FAH SSN VG M T L LEQ K MG D AT W LD Y LN R F G V P T R F G L T D E Y A G	360
Query	436	QL PAD NIV NIA QSS FG QG I S V T Q T Q M I R A F T A I A N D G V M L E P K F I S A I Y D P N D Q T A R K S Q	495
Sbjct	361	QL PAD NIV NIA QSS FG QG I S V T Q T Q M I R A F T A I A N D G V M L E P K F I S A I Y D P N D Q T A R K S Q	420

Query	496	KEIVGNPVSKDAASLRTTNMVLVGTDPVYGTMYNHSTGKPTVTVPQNVALKSGTAQIAD	555
Sbjct	421	KEIVGNPVSKDAASLRTTNMVLVGTDPVYGTMYNHSTGKPTVTVPQNVALKSGTAQIAD	480
Query	556	EKNGGYLVGLTDYIFSAVSMSPAENPDFILYTVVQQPEHYSGIQLGEFANPILERASAMK	615
Sbjct	481	EKNGGYLVGLTDYIFSAVSMSPAENPDFILYTVVQQPEHYSGIQLGEFANPILERASAMK	540
Query	616	DSLNLOTTAKALEQVSQQSPYPMPSVKDISPGDLAEEELRRNLVQPIVVGTGKIKNNSAE	675
Sbjct	541	DSLNLOTTAKALEQVSQQSPYPMPSVKDISPGDLAEEELRRNLVQPIVVGTGKIKNNSAE	600
Query	676	EGKNLAPNQQVLILSDKAEEVPDMYGWTKETAETLAKWLNLIELEFQGSGSTVQKQDVRAN	735
Sbjct	601	EGKNLAPNQQVLILSDKAEEVPDMYGWTKETAETLAKWLNLIELEFQGSGSTVQKQDVRAN	660
Query	736	TAIKDIKKITLTLGD 750	
Sbjct	661	TAIKDIKKITLTLGD 675	

>gb|AAC45547.1| low-affinity penicillin-binding protein 2X [Streptococcus pneumoniae]
Length=750

Score = 1284 bits (3323), Expect = 0.0, Method: Composition-based stats.
Identities = 654/750 (87%), Positives = 704/750 (93%), Gaps = 0/750 (0%)

Query	1	MKWTKR VIRYAT KNRK SPAEN RRRVGK SLLS VFVFAI F L V N F AVI I G T G T R F G T D L A K MKWTKR+ R+A +NRKSPAENR+ VKG +SLL+V +FA+FLVNFAVIIG+G++FGTDL K	60
Sbjct	1	MKWTKR IT R FAIR NRK SPAEN RK I VG KYI SLLA V VL F AV F L V N F AVI I G S G S K F G T D L V K	60
Query	61	EAKKVHQ QTTR TVPAKRG TI YDRNGVPIAEDATSYN VYAVIDEN YKSATG K I LYVEKTQFN EAKKVHQ TRT VPAKRG TI YDRNGVPIAEDATSYN VYAVID+ YKSATG K I LYVE QFN	120
Sbjct	61	EAKKVHQ I TRT VPAKRG TI YDRNGVPIAEDATSYN VYAVIDK K YKSATG K I LYVEDA QFN	120
Query	121	KVAEV FHK YLDMEESVYVREQLSQPNLKQVSFGAKGN GITYANMMSIKKELEAAEVKGIDF KVAEV FHK YLDMEESVYVREQLSQPNLKQVSFG+KGN GITYANMM+IKKELE AEVKGIDF	180
Sbjct	121	KVAEV FHK YLDMEESVYVREQLSQPNLKQVSFGSKGN GITYANMMAIKKELEAEVKGIDF	180
Query	181	TTSPNRSYPNGQFASSFIGLAQHLHENEDGSKSLLGTSGMESSLNSILAGTDGIITYEKDR TTSPNRSYPNGQFASSFIGLAQHLHENEDGSKSLLGTSGMESSLNSILAGTDGIITYEKDR	240
Sbjct	181	TTSPNRSYPNGQFASSFIGLAQHLHENEDGSKSLLGTSGMESSLNSILAGTDGIITYEKDR	240
Query	241	LGNIVPGTEQVSQRTMDGKD VYTTI SSPLQS FMETQMDAFQEKVKGKYMTATL VS AKT GE +GNIVPGTE VSQ+T+DGKD VYTT+SSPLQS FMETQMDAF EKVKGKYMTATL VS AKT GE	300
Sbjct	241	VGNIVPGTEL V SQQTVDGKD VYTTLSSPLQS FMETQMDAFLEKVKGKYMTATL VS AKT GE	300
Query	301	I LAT TQRPTFDADTKEG I TED FVWRD I LYQSN YEPG STMKV MMLAAAIDNNTFP GGEV FN I LAT TQRPTF+ADTKEG I TED FVWRD I LYQSN YEPG S MKVM LA+IDNNTFP GE FN	360
Sbjct	301	I LAT TQRPTFNADTKEG I TED FVWRD I LYQSN YEPG SAMKV MTLASSIDNNTFPSGEY FN	360
Query	361	SSELKIADATI RDWDVNEGLTGGRMMTFSQGFAHSSNVGM T LLEQKMGDATWLDYLNRFK SSE KIADAT RDWDVNEGLT G MMFT QGFAHSSNVGM+LLEQKMGDATWLDYL RFK	420
Sbjct	361	SSEFKIADATTRDWDVNEGLTGGRMMTFLQGFAHSSNVGMSLLEQKMGDATWLDYLKR FK	420
Query	421	FGVPTRFGLTDEYAGQLPADNIVNIAQSSFGQG I SVTQ TQM I R AFTAI ANDGVMLEPKFI FGVPTRFGLTDEYAGQLPADNIV+IAQSSFGQG I SVTQ TQM+RAFTA I ANDGVMLEPKFI	480
Sbjct	421	FGVPTRFGLTDEYAGQLPADNIVSIAQSSFGQG I SVTQ TQM I R AFTAI ANDGVMLEPKFI	480
Query	481	SAI YDPNDQTARKS QKEI VGNPVSKDAASLRTTNMVLVGTDPVYGT MYNHSTGKPTVTVP SAI YD N+Q+ RKS QKEI VGNPVSK+AAS TR +M+LVG TD P+Y GT MYNH TGKP +TVP	540
Sbjct	481	SAI YDTNNQSVRK S QKEI VGNPVSK EAA STTRN HMI LVGTDPLYGT MYNH T GKP II T VP	540
Query	541	GQNVALKSGTAQIADEKNGGYLVGLTDYIFSAVSMSPAENPDFILYTVVQQPEHYSGIQL GQNVA+KSGTAQIADEKNGGYLVG T+Y IFS AV+M+PAENPDFILYTVVQQPEHYSGIQL	600
Sbjct	541	GQNVA V KSGTAQIADEKNGGYLVG ST NYI FSAV TMNP AENPDFILYTVVQQPEHYSGIQL	600
Query	601	GEFANPILERASAMKDSL NLQTTAKALEQVSQQSPYPMPSVKDISPGDLAEEELRRNLVQP GEFA PILERASAMK+SLNLQ+ AK L++V+ +S Y MPS+KDISPG+LAE LRRN+VQP	660
Sbjct	601	GEFATPILERASAMKESLN LQSPAKNL DKV TESSYAMPSIKDISPGELAEALRRNIVQP	660
Query	661	IVVGTG T KIKNSSAEEGKNLAPNQVLILSDKAEEVPDMYGWT KETAETLAKWLNLIELEF IVVGTG T KIK+S EEG NLAPNQVL+LSDK EE+PD MYGW KETAET AKWL+IELEF	720
Sbjct	661	IVVGTG T KIKETSVEEGTNLAPNQVLLSDKV E EIPDMY GWK KETAETFAKWL DIELEF	720
Query	721	QGSGSTVQKQDVRANTAI KDIKKITLTLGD 750 +GSGS VQKQDVR NTAIK+IKKI LT LGD	
Sbjct	721	EGSGSVVQKQDVRNTAI KNIKKIKLT LGD 750	

>dbj|BAD00915.1| penicillin-binding protein 2X [Streptococcus pneumoniae]
Length=750

Score = 1279 bits (3310), Expect = 0.0, Method: Composition-based stats.
Identities = 651/750 (86%), Positives = 702/750 (93%), Gaps = 0/750 (0%)

Query	1	MKWTKR VIRYATK NRK SPAEN RRRVGKSL SLLSVFVFAI F L VNF AVI I GTGTRFGTDLAK MKWTKR+ R+A +NRK SPAENR+ VKG +SLL+V +FA+FLVNFAVIIG+G++FGTDL K	60
Sbjct	1	MKWTKR IT RFAIR NRK SPAENR KIVGKYI SLLAVVLFAVFLVNFAVIIGSGSKFGTDLVK	60
Query	61	EAKKVHQ TTRVPAKRG TI YDRNGVPIAEDATSYN VYAVIDEN YKSATG KILYVEKTQFN EAKKVHQ TRTVP A KRG TI YDRNGVPIAEDATSYN VYAVID+ YKSATG KILYVE QFN	120
Sbjct	61	EAKKVHQ ITRVPAKRG TI YDRNGVPIAEDATSYN VYAVIDKKYKSATG KILYVEDAQFN	120
Query	121	KVAEV FH KYL DMEES YVREQLSQPNL KQV SFGAKGN GITYANMMSIKKELEAAEVKGIDF KVAEV FH KYL DMD+E+YV+EQLSQPNL QVSFGAKGN GITYANMM+IKKELE AEVKGIDF	180
Sbjct	121	KVAEV FH KYL DMEAYVKEQLSQPNLTQVSFGAKGN GITYANMMAIKKELEAEVKGIDF	180
Query	181	TTSPNRSY PNGQFASSFIGLAQLHENE DGSK SLLGTSGMESSLNSILAGTDGIITYEKDR TTSPNRSY PNGQFASSFIGLAQLHENE DGSK SLLGTSGMESSLNSILAG DGIITYEKDR	240
Sbjct	181	TTSPNRSY PNGQFASSFIGLAQLHENE DGSK SLLGTSGMESSLNSILAGKDGIITYEKDR	240
Query	241	LGNIVPGTEQVSQRTMDGKD VYT TISSPLQSF METQMDAFQEKVKGKYM TATL VS A KTG E LGNIVPGTEQVSQ+T+DGKD VYT+SSPLQSF METQMDAF EKVVKGKYM TATL VS A KTG E	300
Sbjct	241	LGNIVPGTEQVSQQTVDGKD VYT TLSSPLQSF METQMDAFLEKVKGKYM TATL VS A KTG E	300
Query	301	I LATTQRPTFDADTKEGI TEDFVWRDILYQS NYEPGSTMKVMM LAAI DNNTFPGEVFN I LATTQRPTF+ADTKEGI TEDFVWRDILYQS NYEPGS KVMM LA++IDNNTFP GE FN	360
Sbjct	301	I LATTQRPTFNADTKEGI TEDFVWRDILYQS NYEPGS AFKVMM LASSIDNNTFPSGEYFN	360
Query	361	SSELKIADATI RDWDVNEGLTGGRMM TFSQGFAHSSNVGM TLEQKMGDATWL DYL NRFK SSE KIADAT RDWDVNEGLT G MMTFSQGFAHSSNVG +LLEQKMGDATWL DYL RFK	420
Sbjct	361	SSEFKIADATTRDWDVNEGLTGGM MTFSQGFAHSSNVG TSLL EQKMGDATWL DYL KRFK	420
Query	421	FGVPTRFGLTDEYAGQLPADNIVNIAQSSFGQG I SVTQ TQMRAFTA I ANDGVML EPKFI FGVPTRFGLTDEYAGQLPADNIV+IAQSSFGQG I SVTQ TQM+RAFTA I ANDGVML EPKFI	480
Sbjct	421	FGVPTRFGLTDEYAGQLPADNIVSIAQSSFGQG I SVTQ TQMRAFTA I ANDGVML EPKFI	480
Query	481	SAIYDPNDQTARKS QKEI VGNP VSKDAAS LTR TNMVL VGTDPV YGT MYH STG KPTV T VP SAIYD N+Q+ RKS QKEI VGNP VSK+AAS TR +M+LVGTDP+YGT MYH TGKP +TVP	540
Sbjct	481	SAIYDTNNQSVRK S QKEI VGNP VSK EAAS TR RNHM ILVGTDPYGT MYH TGKPIIT VP	540
Query	541	GQNVALKSGTAQIADEKNGGYLVGLTDYIFSAV S MS PAEN P DFI LYVTVQ QPEH YSGIQL GQNVA+KSGTAQIADEKNGGYLVG T+YIFS V+M+PAEN P DFI LYVTVQ QPEH YSGIQL	600
Sbjct	541	GQNVAV KSGTAQIADEKNGGYLVG STNYIFSVVTMNP AEN P DFI LYVTVQ QPEH YSGIQL	600
Query	601	GEFANPILERASAMKDSLNLQTTAKALEQV SQQSPYPMPSV KDI SPGD LAEELRRN LVQP GEFA PILERASAMK+SLN LQ+ AK L++V+ +S Y MPS+KDI SPG+LAE LRRN+VQP	660
Sbjct	601	GEFATPILERASAMKESLN LQSPAKNLDKV TESSYAMPSIKD I SPGELAEALRRN IVQP	660
Query	661	I VVGTGTKIKNSSAEEGKNLAPNQQLI LSDKAEEV PDMYGW T KETAETLAKWL NIELEF I VVGTGTKI K+S EEG NLAPNQQL+LSDK EE+PDMYGW KETAET AKWL+IELEF	720
Sbjct	661	I VVGTGTKI KETSVEEGTNLAPNQQLLSDK VEEI PDMYGW KETAETFAKWL DIELEF	720
Query	721	QGSGSTVQKQDVR RANTAI KDI KIT LT LGD 750 +GSGS VQKQDVR NTAIK+IKKI LT LGD	750
Sbjct	721	EGSGS VVQKQDVR NT A I KN KIK LT LGD 750	750

>dbj|BAD00940.1| penicillin-binding protein 2X [Streptococcus pneumoniae]
Length=750

Score = 1275 bits (3300), Expect = 0.0, Method: Composition-based stats.
Identities = 647/750 (86%), Positives = 702/750 (93%), Gaps = 0/750 (0%)

Query	1	MKWTKR VIRYATK NRK SPAEN RRRVGKSL SLLSVFVFAI F L VNF AVI I GTGTRFGTDLAK MKWTKR+ R+A +NRK SPAENR+ VKG +SLL+V +FA+FLVNFAVIIG+G++FGTDL K	60
Sbjct	1	MKWTKR IT RFAIR NRK SPAENR KIVGKYI SLLAVVLFAVFLVNFAVIIGSGSKFGTDLVK	60
Query	61	EAKKVHQ TTRVPAKRG TI YDRNGVPIAEDATSYN VYAVIDEN YKSATG KILYVEKTQFN EAKKVHQ TRTVP A KRG TI YDRNGVPIAEDATSYN VYAVID+ YKSATG KILYVE QFN	120
Sbjct	61	EAKKVHQ ITRVPAKRG TI YDRNGVPIAEDATSYN VYAVIDKKYKSATG KILYVEDAQFN	120
Query	121	KVAEV FH KYL DMEES YVREQLSQPNL KQV SFGAKGN GITYANMMSIKKELEAAEVKGIDF KVAEV FH KYL DMD+E+YV+EQLSQPNL QVSFGAKGN GITYANMM+IKK+L+ A V+GIDF	180
Sbjct	121	KVAEV FH KYL DMEAYVKEQLSQPNLTQVSFGAKGN GITYANMMAIKKDLKDASVEGIDF	180
Query	181	TTSPNRSY PNGQFASSFIGLAQLHENE DGSK SLLGTSGMESSLNSILAGTDGIITYEKDR TTSPNRSY PNGQFASSFIGLAQLHENE DGSK SLLGTSGMESSLNSILAG DGIITYEKDR	240
Sbjct	181	TTSPNRSY PNGQFASSFIGLAQLHENE DGSK SLLGTSGMESSLNSILAGKDGIITYEKDR	240
Query	241	LGNIVPGTEQVSQRTMDGKD VYT TISSPLQSF METQMDAFQEKVKGKYM TATL VS A KTG E LGNIVPGTEQVSQ+T+DGKD VYT+SSPLQSF ME+QMDAFQEK+KGKYM TATL VS A KTG E	300
Sbjct	241	LGNIVPGTEQVSQQTVDGKD VYT TLSSPLQSF MESQMDAFQEKLGKYM TATL VS A KTG E	300
Query	301	I LATTQRPTFDADTKEGI TEDFVWRDILYQS NYEPGSTMKVMM LAAI DNNTFPGEVFN I LATTQRPTF+ADTKEGI TEDFVWRDILYQS NYEPGS MKVM LA++IDNNTFP GE FN	360
Sbjct	301	I LATTQRPTFDADTKEGI TEDFVWRDILYQS NYEPGS AMKVMT LASSIDNNTFPSGEYFN	360
Query	361	SSELKIADATI RDWDVNEGLTGGRMM TFSQGFAHSSNVGM TLEQKMGDATWL DYL NRFK SSE KIADAT RDWDVNEGLT G MMTFSQGFAHSSNVGM+LLEQKMGDATWL DYL RFK	420

NCBI Blast:PBP2X-R6

Sbjct	361	SSEFKIADATTRDWDVNEGLTTGGMMTFLQGFAHSSNVGMSLLEQKMGDATWLDYLKRFK	420
Query	421	FGVPTRFGLTDEYAGQLPADNIVNIAQSSFGQGISVTQTQMIRRAFTAIANDGVMLEPKFI	480
Sbjct	421	FGVPTRFGLTDEYAGQLPADNIV+IAQSSFGQGISVTQTQM+RAFTAIANDGVMLEPKFI	480
Query	481	SAIYDPNDQTARKSQKEIVGNPVS SKDAASLRTNMVLVGTDPVY GTMYNHSTGKPTVTVP SAIYD N+Q+ RKSQKEIVGNPVS K+AAS TR +M+LVGTD P+YGTMYNH TGKP +TVP	540
Sbjct	481	SAIYDTNNQSVRKSQKEIVGNPVS KEA STTRN HMLVGTDP LYGT MYNH TGP II TVP	540
Query	541	GQNVALKSGTAQIADEKNGGYLVGLTDYIFSAVSMSPAENPDFILYVTVQQPEHYSGIQL	600
Sbjct	541	GQNVA+KSGTAQIADEKNGGYLVG T+YIFS V+M+PAENPDFILYVTVQQPEHYSGIQL	600
Query	601	GEFANPILERASAMKDSLNLQTTAKALEQVSQQSPYPMPSVKDISPGDLAEELRRNLVQP	660
Sbjct	601	GEFA PILERASAMK+SLNLQ+ AK L++V+ +S Y MPS+KDISPG+LAE LRRN+VQP	660
Query	661	IVVGTGTKIKNSSAEEGKNLAPNQQVLILSDKAEEV PDMY GWT KETAET AKWL NIELEF	720
Sbjct	661	IVVGTGTKIK+S EEG NLAPNQQVL+LSDK EE+PDMY GW KETAET AKWL+IELEF	720
Query	721	QGSGSTVQKQDVR RANTAIKDIKKITLT LGD 750	
Sbjct	721	+GSGS VQKQDVR NTAIK+IKKI LT LGD EGSGS VVQKQDVR NT A IKNIKKIKLT LGD 750	

>gb|AY56845.1| penicillin-binding protein 2X [Streptococcus pneumoniae]
Length=666

Score = 1271 bits (3290), Expect = 0.0, Method: Composition-based stats.
Identities = 664/666 (99%), Positives = 664/666 (99%), Gaps = 0/666 (0%)

Query	82	RNGVPIAEDATSYNVAVIDENYSATGKILYVEKTQFNKVAEVFH KYLDMEESYVREQL	141
Sbjct	1	RNGVPIAEDATSYNVAVIDENYSATGKILYVEKTQFNKVAEVFH KYLDMEESYVREQL	60
Query	142	SQPNLKQVSFGAKGNGITYANMMSIKKELEAAEVKGIDFTTSPNRSPNGQFASSFIGLA	201
Sbjct	61	SQPNLKQVSFGAKGNGITYANMMSIKKELEAAEVKGIDFTTSPNRSPNGQFASSFIGLA	120
Query	202	QLHENEDGSKSLLGTMGESSLNSILAGTDGIITYEKDRLGNIVPGTEQVSQRTMDGKD	261
Sbjct	121	QLHENEDGSKSLLGTMGESSLNSILAGTDGIITYEKDRLGNIVPGTEQVSQRTMDGKD	180
Query	262	YTTISSLQSFMETQMDAFQE KVKGKYM TATL VS A K TGEI LATT QRP F DAD TKEG I T E D	321
Sbjct	181	YTTISSLQSFMETQMDAFQE KVKGKYM TATL VS A K TGEI LATT QRP F DAD TKEG I T E D	240
Query	322	FVWRDILYQSNYE PGSTMKV MMLAAAIDNNTFPGEVFNSSELKIADATIR DW DVNEG L T	381
Sbjct	241	FVWRDILYQSNYE PGSTMKV M LAAAIDNNTFPGEVFNSSELKIADATIR DW DVNEG L T	300
Query	382	GGRMMTFSQGFAHSSNVG MTLLEQKMG DATWLDYLNRKF GVPTRFGLTDEYAGQLP ADN	441
Sbjct	301	GGRMMTFSQGFAHSSNVG MTLLEQKMG DATWLDYLNRKF GVPTRFGLTDEYAGQLP ADN	360
Query	442	IVNIAQSSFGQGISVTQTQMIRRAFTAI ANDGVMLEPKF ISAIYDPNDQTARKS QKEIVGN	501
Sbjct	361	IVNIAQSSFGQGISVTQTQMIRRAFTAI ANDGVMLEPKF ISAIYDPNDQTARKS QKEIVGN	420
Query	502	PVSKDAASLRTNMVLVGTDPVY GTMYNHSTGKPTVT PGQNVALKSGTAQIADEKNGGY	561
Sbjct	421	PVSKDAASLRTNMVLVGTDPVY GTMYNHSTGKPTVT PGQNVALKSGTAQIADEKNGGY	480
Query	562	L V GLTDYI FSAVSMSPAENPDFILYVTVQQPEHYSGIQLGEFANPILERASAMKDSLNLQ	621
Sbjct	481	L V GLTDYI FSAVSMSPAENPDFILYVTVQQPEHYSGIQLGEFANPILERASAMKDSLNLQ	540
Query	622	TTAKALEQV SQQSPYPMPSVKDISPGDLAEELRRNLVQPIVVG TGT KIKNSSAEEGKNLA	681
Sbjct	541	TTAKALEQV SQQSPYPMPSVKDISPGDLAEELRRNLVQPIVVG TGT KIKNSSAEEGKNLA	600
Query	682	PNQQVLILSDKAEEV PDMY GWT KETAET LAWL NI ELEF FQGS G S T V Q K Q D VR RANTAI KDI	741
Sbjct	601	PNQQVLILSDKAEEV PDMY GWT KETAET LAWL NI ELEF FQGS G S T V Q K Q D VR RANTAI KDI	660
Query	742	KKITL 746	
Sbjct	661	KKITL 665	

>dbj|BAD00908.1| penicillin-binding protein 2X [Streptococcus pneumoniae]
dbj|BAD00911.1| penicillin-binding protein 2X [Streptococcus pneumoniae]
Length=750

Score = 1269 bits (3283), Expect = 0.0, Method: Composition-based stats.
 Identities = 643/750 (85%), Positives = 696/750 (92%), Gaps = 0/750 (0%)

Query	1	MKWTKRVIYATKNRKP SAENRRVGKSL LSVVFVFAIFLVNFAVI IGTGTRGTDLAK	60
Sbjct	1	MKWTEKITRFAIKNRKP SAKNRRIVGKYLSFVA ALFLANFAYIIAKGNIF GTDLVK	60
Query	61	EAKKVHQTTRTVPAK RGTIYDRNGVPIAEDAT SYNVYAVIDENYKSATG KILYVEKTQFN	120
Sbjct	61	EAKKVHQTTRTVPAK RGTIYDRNGVPIAEDAT SYNVYAVID+ YKSATG KILYVE +QFN	120
Query	121	KVAEVFH KYLDMEESYVREQLS QPNLKQVSFGAKGN GITYANMMSIKKELE AAEVKGIDF	180
Sbjct	121	KVAEVFH KYLDMEAYVKEQ LAQPNLTQVSFGAKGN GITYANMMAIKNDL KTAGVEGIDF	180
Query	181	TTSPNRSPNGQF ASSFIGLAQLH ENEDGSKSL TSGMESSLNSI LAGTDGIITYEKDR	240
Sbjct	181	TTSPNRSPNGQF ASSFIGLAQLH ENEDGT KRLIGSS LESSLNSI LAGTDGIITYEKDR	240
Query	241	LGNIVPGTEQ VSQRTMDGKD VYTTISPLQ SFMETQMDA FQEVKVKG KYMATT LVSAKTGE	300
Sbjct	241	LGNIVPGTEQ SQ T+DGK DVT+SSPLQ SFMETQMDA FQEVKVKG KYMATT LVSAKTGE	300
Query	301	ILATTQRPTFD ADTKEGITEDF VWRDILYQSN YEPGSTM KVMMLAAA IDNNNTFP GEVFN	360
Sbjct	301	ILATTQRPTF+ ADTK+GIT+DF VWRDILYQSN YEPGS MKVM LA+IDNNNTFP GE FN	360
Query	361	SSELKIADAT IRDWDVN NEGLTGG RMMTSQG FAHSSNV GMTLLEQ KMGDATA WLDYLNRFK	420
Sbjct	361	SSELKIADAT IRDWDVN+GLT G MMTFSQG FAHSSNV GM+LLEQ KMGDATA WLDYLNRFK	420
Query	421	FGVPTRFGLT DEYAGQLP ADNIVNIA QSSFGQ ISVTQTQ MIRAFTA IANDGV MLEPKFI	480
Sbjct	421	FGVPTRFGLT DEY GQLP ADNIVNIA S+FGQ GISVTQTQ MIRAFTA IANDGV MLEPKFI	480
Query	481	SAIYDPND QTARKS QKEIVGN PVSKDA ASLRT TNMV LVTG DPVY GTM YNH STG KPT TV VP	540
Sbjct	481	SAIYDPND QSVRK SQKEIVGN PVSKAA ASSTREHM VMVG TDPV YGT MYNH STG KPN NVNP VP	540
Query	541	GQNVALK SGTAQIA DEKNGGY LVGLTDY IFSAV SMSPA ENPDF ILYV TVQQ PEHY SGIQL	600
Sbjct	541	GQNVALK SGTAQIA DEKNGGY L G T+Y IFS VSM PAENPD FILYV TVQQ PEHY SGVQL	600
Query	601	GEFAN PILE RASAM KDSL NLQTT AKALE QVS QQSP YPMPS VKDI SPGD LAE LRRN VQP	660
Sbjct	601	GEFAN PILE RASAMK+ SLNLQ+ AK L++V+ +S Y MPS+K DISPG+LAE LRRN+VQP	660
Query	661	IVVGTG TKIKN SSAEG GKLN APN QQVL IL SDK KAEE VPD MYG WT KETA ET LAK WL NIE LEF	720
Sbjct	661	IVVGTG TKIK SS EEG NL APN QQVL+ LSDK EE+ PDMY GW KETA ET AK WL+IE LEF	720
Query	721	QGSG STVQ KQDV RANT AIK DIKK ITL LGD	750
Sbjct	721	+GSGS VQK QDVR N TAIK+ IKKI L LGD	750

>gb|ABB46504.1| penicillin binding protein 2x [Streptococcus pneumoniae]
 gb|ABB46507.1| penicillin binding protein 2x [Streptococcus pneumoniae]
 Length=657

Score = 1258 bits (3254), Expect = 0.0, Method: Composition-based stats.
 Identities = 656/657 (99%), Positives = 657/657 (100%), Gaps = 0/657 (0%)

Query	94	YNYAVI DENYKSATG KILYVEK TQFNKVAE VFHKYLD MEESYVRE QLSQPNL KQVSFGA	153
Sbjct	1	YNYAVI DENYKSATG KILYVEK TQFNKVAE VFHKYLD MEESYVRE QLSQPNL KQVSFGA	60
Query	154	KGN GITYAN MMSIK KELEAA EVKGID FTTSPN RSYPNG QFASSFIG LAQLHE NEDGSK SL	213
Sbjct	61	KGN GITYAN MMSIK KELEAA EVKGID FTTSPN RSYPNG QFASSFIG LAQLHE NEDGSK SL	120
Query	214	LGT SGMESS LNSI LAGTD GII TYEK DRLGN IVPG TEQV SQR TMG KD VYT TIS SPLQ SF	273
Sbjct	121	LGT SGMESS LNSI LAGTD GII TYEK DRLGN IVPG TEQV SQR TMG KD VYT TIS SPLQ SF	180
Query	274	ETQMDA FQE VKKG KYM TATL VSA KTGE ILATT QRPT FDAD TKE GITED FV WRD ILYQ SNY	333
Sbjct	181	ETQMDA FQE VKKG KYM TATL VSA KTGE ILATT QRPT FDAD TKE GITED FV WRD ILYQ SNY	240
Query	334	EPG STM KVM MLAAA IDNN TFPG GEV FNS SEL KIA DAT IRD WDV NEGL TGG RMM TSQ GFA	393
Sbjct	241	EPG STM KVM MLAAA IDNN TFPG GEV FNS SEL KIA DAT IRD WDV NEGL TGG RMM TSQ GFA	300
Query	394	HSSNV GMLLE QKM GDA TLD LNR FKFG VPT RGLT DEY AGQ LPAD NIV NIA QSS FGQG	453
Sbjct	301	HSSNV GMLLE QKM GDA TLD LNR FKFG VPT RGLT DEY AGQ LPAD NIV NIA QSS FGQG	360

Query	454	ISVTQTOQMIRAFTAIANDGVMLEPKFISAIYDPNDQTARKS0KEIVGNPVSCKDAASLT	513
Sbjct	361	ISVTQTOQMIRAFTAIANDGVMLEPKFISAIYDPNDQTARKS0KEIVGNPVSCKDAASLT	420
Query	514	NMVLVGTDPVYGTMYNHNSTGKPTVTPGQNVALKSGTAQIADEKNGGYLVGLTDYIFSAV	573
Sbjct	421	NMVLVGTDPVYGTMYNHNSTGKPTVTPGQNVALKSGTAQIADEKNGGYLVGLTDYIFSAV	480
Query	574	SMSPAENPDFILYVTVQQPEHYSGIQLGEFANPILERASAMKDSLNLOTTAKALEQVSQQ	633
Sbjct	481	SMSPAENPDFILYVTVQQPEHYSGIQLGEFANPILERASAMKDSLNLOTTAKALEQVSQQ	540
Query	634	SPYPMPMSVKDISPGDLAEEELRRNLVQPIVVGTGKIKNSSAEGKNLAPNQQVLILSDKA	693
Sbjct	541	SPYPMPMSVKDISPGDLAEEELRRNLVQPIVVGTGKIKNSSAEGKNLAPNQQVLILSDKA	600
Query	694	EEVPDMYGTWTKETAETLAKWLNLIEFQGSGSTVQKQDVRVANTAIKDIKKITLTD	750
Sbjct	601	EEVPDMYGTWTKETAETLAKWLNLIEFQGSGSTVQKQDVRVANTAIKDIKKITLTD	657

>gb|AAN32862.1| penicillin-binding protein 2X [Streptococcus pneumoniae]
Length=661

Score = 1235 bits (3195), Expect = 0.0, Method: Composition-based stats.
Identities = 643/661 (97%), Positives = 652/661 (98%), Gaps = 0/661 (0%)

Query	90	DATSYNVYAVIDENYSATGKILYVEKTQFNKVAEVFKYLDMEESYVREQLSQPNLKQV	149
Sbjct	1	DATSYNVYAVIDENYSATGKILYVEKTQFNKVAEVFKYLDMEESYVREQLSQPNLKQV	60
Query	150	SFGAKGNGITYANMMSIKKELEAAEVKGIDFTTSPNRSYPNGQFASSFIGLAQLHENEDG	209
Sbjct	61	SFG+KGNIGITYANMMSIKKELE AEVKGIDFTTSPNRSYPNGQFASSFIGLAQLHENEDG	120
Query	210	SKSLLGTSGMESSLNSILAGTDGIITYEKDRGNIVPGTEQVSQRTMDGKDVTISSL	269
Sbjct	121	SKSLLGTSGMESSLNSILAGTDGIITYEKDRGNIVPGTEQVSQ+T+DGKDVTISSL	180
Query	270	QSFMETQMDAFQEKVKGKYMTATLVSAKTGEILATTQRPTFDADTKEGITDFVWRDILY	329
Sbjct	181	QSFMETQMDAFQEKVKGKYMTATLVSAKTGEILATTQRPTFDADTKEGITDFVWRDILY	240
Query	330	QSNYEPGSTMKVMMALAAIDNNTFPGGEVFNSSELKIADATIRDWDVNNEGLTGGGRMMTF	389
Sbjct	241	QSNYEPGS MKVM LAAAIDNNTFPGGEVFNSSELK+AD T RDWDVNNEGLTGG MMTFS	300
Query	390	QGFAHSSNVGMTLLEQKMGDATWLDYLNRFKFGVPTRFGLTDEYAGQLPADNIVNIAQSS	449
Sbjct	301	QGFAHSSNVGMTLLEQKMGDATWLDYLNRFKFGVPTRFGLTDEYAGQLPADNIVNIAQSS	360
Query	450	FGQGISVTQTOQMIRAFTAIANDGVMLEPKFISAIYDPNDQTARKS0KEIVGNPVSCKDAAS	509
Sbjct	361	FGQGISVTQTOQMIRAFTAIANDGVMLEPKFISAIYDPNDQTARKS0KEIVGNPVSCKDAAS	420
Query	510	LTRTNMVLVGTDPVYGTMYNHNSTGKPTVTPGQNVALKSGTAQIADEKNGGYLVGLTDYI	569
Sbjct	421	LTRTNMVLVGTDPVYGTMYNHNSTGKPTVTPGQNVALKSGTAQIADEKNGGYLVGLTDYI	480
Query	570	FSAVSMSPAENPDFILYVTVQQPEHYSGIQLGEFANPILERASAMKDSLNLOTTAKALEQ	629
Sbjct	481	FSAVSM+PAENPDFILYVTVQQPEHYSGIQLGEFANPILERASAMKDSLNLOTTAKALEQ	540
Query	630	VSQQSPYPMPSVKDISPGDLAEEELRRNLVQPIVVGTGKIKNSSAEGKNLAPNQQVLIL	689
Sbjct	541	VSQQSPYPMPSVKDISPGDLAEEELRRNLVQPIVVGTGKIKNSSAEGKNLAPNQQVLIL	600
Query	690	SDKAEEVPDMYGTWTKETAETLAKWLNLIEFQGSGSTVQKQDVRVANTAIKDIKKITLTD	749
Sbjct	601	SDKAEEVPDMYGTWTKETAETLAKWLNLIEFQGSGSTVQKQDVRVANTAIKDIKKITLTD	660
Query	750	D 750	
Sbjct	661	D 661	

>gb|AAN32857.1| penicillin-binding protein 2X [Streptococcus pneumoniae]
gb|AAN32858.1| penicillin-binding protein 2X [Streptococcus pneumoniae]
Length=661

Score = 1234 bits (3194), Expect = 0.0, Method: Composition-based stats.
Identities = 643/661 (97%), Positives = 653/661 (98%), Gaps = 0/661 (0%)

Query	90	DATSYNVYAVIDENYSATGKILYVEKTQFNKVAEVFKYLDMEESYVREQLSQPNLKQV	149
Sbjct		DATSYNVYAVIDENYSATGKILYVEKTQFNKVAEVFKYLDMEESYVREQLSQPNLKQV	

- Sbjct	1	DATSYNVYAVIDENYKSATGKILYVEKTQFNKVAEVFH KYLDMEESYVREQLSQPNLKQV	60
Query	150	SFGAKGNIGINANMMSIKKELEAAEVKGIDFTTSPNRSPNGQFASSFIGLAQLHENEDG	209
- Sbjct	61	SFGAKGNIGINANMMSIKKELE AEVKGIDFTTSPNRSPNGQFASSFIGLAQLHENEDG	120
Query	210	SKSLLGTSGMESSLNSILAGTDGIITYEKDRLGNIVPGTEQVSQRTMDGKDVTISSL	269
Sbjct	121	SKSLLGTSGMESSLNSILAGTDGIITYEKDRLGNIVPGTEQISQQTVDGKDVTISSL	180
Query	270	QSFMETQMDAFQEVKVGKYMATTLSAKTGEILATTQRPTFDADTKEGITEDFVWRDILY	329
Sbjct	181	QSFMETQMDAFQEVKVGKYMATTLSAKTGEILATTQRPTF+ADTKEGIT+DFVWRDILY	240
Query	330	QSNYEPGSTMVKVMMALAAIDNNTFPGGEVFNSELKIADATIRDWDVNNEGLTGGRMMTFS	389
Sbjct	241	QSNYEPGS MKVM LAA+IDNNTFPGGE FNSSELKIAD TIRDWDVNNEGLTG MMTFS	300
Query	390	QGFAHSSNVGMTLLEQKMGDATWLDYLNRFKFGVPTRFGLTDEYAGQLPADNIVNIAQSS	449
Sbjct	301	QGFAHSSNVGMTLLEQKMGDATWLDYLNRFKFGVPTRFGLTDEYAGQLPADNIVNIAQSS	360
Query	450	FGQQGISVTQTMIRAFTAIANDGVMLEPKFISAIYDPNDQTARKSQKEIVGNPVS KDAAS	509
Sbjct	361	FGQQGISVTQTMIRAFTAIANDGVMLEPKFISAIYDPNDQTARKSQKEIVGNPVS KDAAS	420
Query	510	LTRTNMVLVGTDPVYGTMYNHSTGKPTVTPGQNVALKSGTAQIADEKNGGYLVGLTDYI	569
Sbjct	421	LTRTNMVLVGTDPVYGTMYNHSTGKPTVTPGQNVALKSGTAQIADEKNGGYLVGLT+YI	480
Query	570	FSAVSMSPAENPDFILYVTVQQPEHYSGIQLGEFANPILERASAMKDSLNLQTTAKALEQ	629
Sbjct	481	FSAVSMSPAENPDFILYVTVQQPEHYSGIQLGEFANPILERASAMKDSLNLQTTAK+LEQ	540
Query	630	VSQQSPYPMPSVKDISPGDLAELRRNLVQPIIVVGTGKIKNSSAEEGKNLAPNQQLIL	689
Sbjct	541	VSQQSPYPMPSVKDISPGDLAELRRNLVQPIIVVGTGKIKNSSAEEGKNLAPNQQLIL	600
Query	690	SDKAEEVPDMYWTKETAETLAKWLNLIELEFQGSGSTVQKQDVRANTAIKDIKKITLTG	749
Sbjct	601	SDKAEEVPDMYWTK TAET AKWLNLIELEF+GSG+TVQKQDVRANTAIKDIKKITLTG	660
Query	750	D 750	
Sbjct	661	D 661	

>emb|CAB65447.1| penicillin binding protein 2x [Streptococcus pneumoniae]
Length=666

Score = 1230 bits (3182), Expect = 0.0, Method: Composition-based stats.
Identities = 639/666 (95%), Positives = 653/666 (98%), Gaps = 0/666 (0%)

Query	85	VPIAEDATSYNVYAVIDENYKSATGKILYVEKTQFNKVAEVFH KYLDMEESYVREQLSQP	144
Sbjct	1	VPIAEDATSYNVYAVIDENYKSATGKILYVEKTQFNKVAEVFH KYLDMEESYVREQLSQP	60
Query	145	NLKQVSGAKGNIGINANMMSIKKELEAAEVKGIDFTTSPNRSPNGQFASSFIGLAQLH	204
Sbjct	61	NLKQVSGAKGNIGINANMMSIKKELE AEVKGIDFTTSPNRSPNGQFASSFIGLAQLH	120
Query	205	ENEDGSKSLLGTSMESSLNSILAGTDGIITYEKDRLGNIVPGTEQVSQRTMDGKDVTI	264
Sbjct	121	ENEDGSKSLLGTSMESSLNSILAGTDGIITYEKDRLGNIVPGTEQVSQ+T+DGKDVTI	180
Query	265	ISSPLQSFMETQMDAFQEVKVGKYMATTLSAKTGEILATTQRPTFDADTKEGITEDFVW	324
Sbjct	181	ISSPLQSFMETQMDAFQEVKVGKYMATTLSAKTGEILATTQRPTFDADTKEGITEDFVW	240
Query	325	RDILYQSNYEPGSTMVKVMMALAAIDNNTFPGGEVFNSELKIADATIRDWDVNNEGLTGGR	384
Sbjct	241	RDILYQSNYEPGSTMVKVMMALAAIDNNTFPGGEVFNSELKIADATIRDWDVNNEGLTGGR	300
Query	385	MMTFSQGFAHSSNVGMTLLEQKMGDATWLDYLNRFKFGVPTRFGLTDEYAGQLPADNIVN	444
Sbjct	301	MMTFSQGFAHSSNVGMTLLEQKMGDATWLDYLNRFKFGVPTRFGLTDEYAGQLPADNIVN	360
Query	445	IAQSSFGQQGISVTQTMIRAFTAIANDGVMLEPKFISAIYDPNDQTARKSQKEIVGNPVS	504
Sbjct	361	IA S+FGQQGISVTQTM+RAFTAIA ANDGVMLEPKFISA+YDPNDQ+ RKSQKEIVGNPVS	420
Query	505	KDAASLRTNMVLVGTDPVYGTMYNHSTGKPTVTPGQNVALKSGTAQIADEKNGGYLVG	564
Sbjct	421	KEAASVTRDHMV MVGTDPTYGTMYNHSTGKATVN VPGQNVALKSGTAEIADEKNGGYLTG	480
Query	565	LTDYIFSAVMSPAENPDFILYVTVQQPEHYSGIQLGEFANPILERASAMKDSLNLQTTA	624

	T+ IFS VSM PAENPDFILYVTVQQPEHYSQIQLGEFANPILERASAMK+SLNLQTTA	
Sbjct 481	STNNIFSVVSMHPAENPDFILYVTVQQPEHYSQIQLGEFANPILERASAMKESLNQTTA	540
Query 625	KALEQVSQQSPYPMPSVKDISPGDLAEELRRNLVQPIIVVGTGKIKNSSAEEGKNLAPNQ	684
Sbjct 541	KALEQVSQQSPYPMPSVKDISPGDLAEELRRNLVQPIIVVGTGKIKNSSAEEGKNLAPNQ	600
Query 685	QVLILSDKAAEVVPDMYWTKETAETLAKWLNLIELEFGSGSTVQKQDVRANTAIKDIKKI	744
Sbjct 601	QVLILSDKAAEVVPDMYWTKETAETFAKWLNLIELEFGSGSTVQKQDVRANTAIKDIKKI	660
Query 745	TTLGD 750	
Sbjct 661	TTLGD 666	

>gb|AAN32865.1| penicillin-binding protein 2X [Streptococcus pneumoniae]
Length=661

Score = 1222 bits (3161), Expect = 0.0, Method: Composition-based stats.
Identities = 636/661 (96%), Positives = 651/661 (98%), Gaps = 0/661 (0%)

Query 90	DATSYNVYAVIDENYKSATGKILYVEKTQFNKVAEVFKYLDMEESYVREQLSQPNLKQV	149
Sbjct 1	DATSYNVYAVIDENYKSATGKILYVEKTQFNKVAEVFKYLDMEESYVREQLSQPNLKQV	60
Query 150	SFGAKGNIGITYANMMSIKKELEAAEVKGIDFTTSPNRSPNGQFASSFIGLAQLHENEDG	209
Sbjct 61	SFGAKGNIGITYANMMSIKKELEAAEVKGIDFTTSPNRSPNGQFASSFIGLAQLHENEDG	120
Query 210	SKSLLGTSGMESSLNSILAGTDGIITYEKDRLGNIVPGTEQVSQRTMDGKDVTISSL	269
Sbjct 121	SKSLLGTSGMESSLNSILAGTDGIITYEKDRLGNIVPGTEQVSQRTMDGKDVTISSL	180
Query 270	QSFMETQMDAFQEKVKGKYMATTLSAKTGEILATTQRPTFDADTKEGITEDFWRDILY	329
Sbjct 181	QSFMETQMDAFQEKVKGKYMATTLSAKTGEILATTQRPTFDADTKEGITKDFWRDILY	240
Query 330	QSNYEPGSTMVKVMMALAAIDNNTFPGGEVFNSSELKIADATIRDWDVNNEGLTGGRMMTFS	389
Sbjct 241	QSNYEPGSTMVKVMMALAAIDNNTFPGGEVFNSSELKIADATIRDWDVNNEGLTGGRMMTFS	300
Query 390	QGFAHSSNVGMTLLEQKMGDATWLDYLNRFKFGVPTRFGLTDEYAGQLPADNIVNIAQSS	449
Sbjct 301	QGFAHSSNVGMTLLEQKMGDATWLDYLNRFKFGVPTRFGLTDEYAGQLPADNIVNIAQSS	360
Query 450	FGQGISVTQTMIRAFTAIANDGVMLEPKFISAIYDPNDQTARKSQKEIVGNPVSCKDAAS	509
Sbjct 361	FGQGISVTQTMIRAFTAIANDGVMLEPKFISAIYDPNDQTARKSQKE+VGNPVSCKDAAS	420
Query 510	LTRTNMVLVGTDPVYGTMYNHSTGKPTVTPGQNVALKSGTAQIADEKNGGYLVGLTDYI	569
Sbjct 421	LTRTNMVLVGTDPVYGTMYNHSTGKPTVTPGQNVALKSGTA+IADEKNGGYLVG T+ I	480
Query 570	FSAVSMSPAENPDFILYVTVQQPEHYSQIQLGEFANPILERASAMKDSLNQTTAKALEQ	629
Sbjct 481	FSVVAMNPAEDPDFILYVTVQQPEHYSQIQLGEFANPILERASAMKESLNQSPAKNLDK	540
Query 630	VQQSPYPMPSVKDISPGDLAEELRRNLVQPIIVVGTGKIKNSSAEEGKNLAPNQVLIL	689
Sbjct 541	VTESSYAMPSIKDISPGDLAEELRRNLVQPIIVVGTGKIKNSSAEEGKNLAPNQVLIL	600
Query 690	SDKAEEVPDMYWTKETAETLAKWLNLIELEFGSGSTVQKQDVRANTAIKDIKKITLTLG	749
Sbjct 601	SDKAEEVPDMYWTKETAETLAKWLNLIELEFGSGSTVQKQDVRANTAIKDIKKITLTLG	660
Query 750	D 750	
Sbjct 661	D 661	

>emb|CAD90770.1| penicillin-binding protein 2x [Streptococcus pneumoniae]
Length=702

Score = 1217 bits (3150), Expect = 0.0, Method: Composition-based stats.
Identities = 627/702 (89%), Positives = 665/702 (94%), Gaps = 0/702 (0%)

Query 49	GTGTRFGTDLAKEAKKVHQTRTVPAKRGTIYDRNGVPIAEDATSYNVYAVIDENYKSAT	108
Sbjct 1	GTGTRFGTDLAKEAKKVHQTRTVPAKRGTIYDRNGVPIAEDATSYNVYAVIDENYKSAT	60
Query 109	GKILYVEKTQFNKVAEVFKYLDMEESYVREQLSQPNLKQVSFGAKGNIGITYANMMSIKK	168
Sbjct 61	GKILYVEKTQFNKVAEVFKYLDMEESYVREQLSQPNLKQVSFG+KGNGIGITYANMMSIKK	120
Query 169	ELEAAEVKGIDFTTSPNRSPNGQFASSFIGLAQLHENEDGSKSLLGTSGMESSLNSILA	228

Sbjct	121	ELE AEVKGIDFTTSPNRSYPNGQFASSFIGLAQLHENEDGSKSLLGTSGMESSLNSILA ELETAEVKGIDFTTSPNRSYPNGQFASSFIGLAQLHENEDGSKSLLGTSGMESSLNSILA	180
Query	229	GTDGIITYEKDRLGNIVPGTEQVSQRTMDGKDVTYTTISPLQSFMETQMDAFQEKVKGKY GTDGIITYEKDR+GNIVPGTE VSQ+T+DGKDVTYTT+SSPLQSFMETQMDAF EKVKGKY	288
Sbjct	181	GTDGIITYEKDRLGNIVPGTEQVSQQTVDGKDVTYTTLSSPLQSFMETQMDAFLEKVKGKY	240
Query	289	MTATLVSAKTGEILATTQRPTFDADTKEGITEDFVWRDILYQSNYEPGSTMVKVMMIAAI MTATLVSAKTGEILATTQRPTF+ADTKEGITEDFVWRDILYQSNYEPGS MKVM LA++I	348
Sbjct	241	MTATLVSAKTGEILATTQRPTFNADTKEGITEDFVWRDILYQSNYEPGSAMKVMTLASSI	300
Query	349	DNNTPGGEVFNSSELKIADATIRDWDVNNEGLTGGRMMTSQGFAHSSNVGMTLLEQKMG DNNTPGGEVFNSSELKIADATIRDWDVN+GLT G MMTF QGFAHSSNVGM+LLEQKMG	408
Sbjct	301	DNNTPSGEYFNSSEFKIADATTRDWDVNNDGLTGGMMTFLQGFAHSSNVGMSLLEQKMG	360
Query	409	DATWLDYLNRFKFGVPTRFGLTDEYAGQLPADNIVNIAQSSFGQGISVTQTQMLRAFTAI DATWLDYL RFKFGVPTRFGLTDEYAGQLPADNIV+IAQSSFGQGISVTQTQMLRAFTAI	468
Sbjct	361	DATWLDYLKRKFKGVPTRFGLTDEYAGQLPADNIVSIAQSSFGQGISVTQTQMLRAFTAI	420
Query	469	ANDGVMLEPKFISAIYDPNDQTARKSQKEIVGNPVSKDAASLTTRNMVLVGTDPVYGTMY ANDGVMLEPKFISAIYD N+Q+ RKSQKEIVGNPVSK+AAS TR +M+LVGTDP+YGTMY	528
Sbjct	421	ANDGVMLEPKFISAIYDTNNQSVRKSQKEIVGNPVSKAESTTRNHMILVGTDPYGTMY	480
Query	529	NHSTGKPTVTVPQNVALKSGTAQIADEKNGGYLVGLTDYIFSAVSMSPAENPDFILYVT NH TGKP +TVPGQNVAV+KSGTAQIADEKNGGYLVG T+YIFS V+M+PAENPDFILYVT	588
Sbjct	481	NHYTGKPIITVPGQNVAVKSGTAQIADEKNGGYLVGSTNYIFSVVTMNPAENPDFILYVT	540
Query	589	VQQPEHYSIGIQLGEFANPILERASAMKDSLNQTTAKALEQVSQQSPYPMPSVKDISPGD VQQPEHYSIGIQLGEFA PILERASAMK+SLNLQ+ AK L++V+ +S Y MPS+KDISPG+	648
Sbjct	541	VQQPEHYSIGIQLGEFATPILERASAMKESLNQSPAKNLKVTESSYAMPSIKDISPGE	600
Query	649	LAEELRRNLVQPIVVGTGTKIKNNSAEEGKNLAPNQQVLILSDKAEEVPDMYGWTKETA LAE LRRN+VQPIVVGTGTKIK +S EEG NLAPNQQVL+LSDK EE+PDYMW KETA	708
Sbjct	601	LAEALRRNLVQPIVVGTGTKIKETSVEEGTNLAPNQQVLLSDKVEEIPDMYMWKETA	660
Query	709	TLAKWLNLIELEFQGSGSTVQKQDVRANTAIKDIKKITLTLGD 750 T AKWL+IELEF+GSGS VQKQDVR NTAIK+IKKI LTLGD	750
Sbjct	661	TFAKWLNLIELEFEGSGSVVQKQDVRTNTAIKNKKIKLTLGD 702	702

>emb|CAD90771.2| penicillin-binding protein 2x [Streptococcus pneumoniae]
Length=702

Score = 1209 bits (3129), Expect = 0.0, Method: Composition-based stats.
Identities = 622/702 (88%), Positives = 662/702 (94%), Gaps = 0/702 (0%)

Query	49	GTGTRFGTDLAKEAKKVHQTRTVPAKRGTYIYDRNGVPIAEDATSYNVYAVIDENYKSAT GTGTRFGTDLAKEAKKVHQTRTVPAKRGTYIYDRNGVPIAEDATSYNVYAVIDENYKSAT	108
Sbjct	1	GTGTRFGTDLAKEAKKVHQTRTVPAKRGTYIYDRNGVPIAEDATSYNVYAVIDENYKSAT	60
Query	109	GKILYVEKTQFNKVAEVFH KYLDEE SYVREQLSOPNLKQVSGFAKNGNITYANMMSIKK GKILYVEKTQFNKVAEVFH KYLDEE SYVREQLSQPNLKQVSGFAKNGNITYANMM+IKK	168
Sbjct	61	GKILYVEKTQFNKVAEVFH KYLDEE SYVREQLSQPNLKQVSGFAKNGNITYANMMAIKK	120
Query	169	ELEAAEVKGIDFTTSPNRSYPNGQFASSFIGLAQLHENEDGSKSLLGTSGMESSLNSILA +L+ A V+GIDFTTSPNRSYPNGQFASSFIGLAQLHENEDGSKSLLGTSGMESSLNSILA	228
Sbjct	121	DLKDASVEGIDFTTSPNRSYPNGQFASSFIGLAQLHENEDGSKSLLGTSGMESSLNSILA	180
Query	229	GTDGIITYEKDRLGNIVPGTEQVSQRTMDGKDVTYTTISPLQSFMETQMDAFQEKVKGKY G DGIITYEKDRLGNIVPGTEQVSQ+T+DGKDVTYTT+SSPLQSFMETQMDAF EKVKGKY	288
Sbjct	181	GKDGIIITYEKDRLGNIVPGTEQVSQQTVDGKDVTYTTLSSPLQSFMETQMDAFLEKVKGKY	240
Query	289	MTATLVSAKTGEILATTQRPTFDADTKEGITEDFVWRDILYQSNYEPGSTMVKVMMIAAI MTATLVSAKTGEILATTQRPTF+ADTKEGITEDFVWRDILYQSNYEPGS KVMMIA++I	348
Sbjct	241	MTATLVSAKTGEILATTQRPTFNADTKEGITEDFVWRDILYQSNYEPGSAMKVMTLASSI	300
Query	349	DNNTPGGEVFNSSELKIADATIRDWDVNNEGLTGGRMMTSQGFAHSSNVGMTLLEQKMG DNNTPGGEVFNSSELKIADATIRDWDVN+GLT G MMTF QGFAHSSNVGM+LLEQKMG	408
Sbjct	301	DNNTPSGEYFNSSEFKIADATTRDWDVNAGLTTGGMMTFLQGFAHSSNVGTSLLEQKMG	360
Query	409	DATWLDYLNRFKFGVPTRFGLTDEYAGQLPADNIVNIAQSSFGQGISVTQTQMLRAFTAI DATWLDYL RFKFGVPTRFGLTDEYAGQLPADNIV+IAQSSFGQGISVTQTQMLRAFTAI	468
Sbjct	361	DATWLDYLKRKFKGVPTRFGLTDEYAGQLPADNIVSIAQSSFGQGISVTQTQMLRAFTAI	420
Query	469	ANDGVMLEPKFISAIYDPNDQTARKSQKEIVGNPVSKDAASLTTRNMVLVGTDPVYGTMY ANDGVMLEPKFISAIYD N+Q+ RKSQKEIVGNPVSK+AAS TR +M+LVGTDP+YGTMY	528
Sbjct	421	ANDGVMLEPKFISAIYDTNNQSVRKSQKEIVGNPVSKAESTTRNHMILVGTDPYGTMY	480
Query	529	NHSTGKPTVTVPQNVALKSGTAQIADEKNGGYLVGLTDYIFSAVSMSPAENPDFILYVT NH TGKP +TVPGQNVAV+KSGTAQIADEKNGGYLVG T+YIFS V+M+PAENPDFILYVT	588
Sbjct	481	NHYTGKPIITVPGQNVAVKSGTAQIADEKNGGYLVGSTNYIFSVVTMNPAENPDFILYVT	540
Query	589	VQQPEHYSIGIQLGEFANPILERASAMKDSLNQTTAKALEQVSQQSPYPMPSVKDISPGD VQQPEH+SGIQLGEFA PILERASAMK+SLNLQ+ AK L++V+ +S Y MPS+KDISPG+	648
Sbjct	541	VQQPEHFSIGIQLGEFATPILERASAMKESLNQSPAKNLKVTESSYAMPSIKDISPGE	600

NCBI Blast:PBP2X-R6

- Query 649 LAEELRRNLVQPIVVGTGKIKNSSAEEGKNLAPNQQVLILSDKAEEVPDMYGWTKETAE 708
 Sbjct 601 LAEALRRNIVQPIVVGTGKIKETSVEEGTNLAPNQQVLLSDKVEEIPDMYGWKKETAE 660

- Query 709 TLAKWLNLIELEFQGSGSTVQKQDVRANTAIKDIKKITLTLGD 750
 Sbjct 661 TFAKWLNLIELEFEGSGSVVQKQDVRNTAIKNIKIKLTLGD 702

>gb|AY56843.1| penicillin-binding protein 2X [Streptococcus pneumoniae]
 >gb|AY56844.1| penicillin-binding protein 2X [Streptococcus pneumoniae]
 Length=669

Score = 1207 bits (3122), Expect = 0.0, Method: Composition-based stats.
 Identities = 625/669 (93%), Positives = 648/669 (96%), Gaps = 0/669 (0%)

Query 82	RNGVPIAEDATSYNVYAVIDENYKSATGKILYVEKTQFNKVAEVFKYLDMEESYVREQL	141
Sbjct 1	RNGVPIAEDATSYNVYAVIDENYKSATGKILYVEKTQFNKVAEVFKYLDMEESYVREQL	60
Query 142	SQPNLKQVSFGAKGNIGITYANMMSIKKELEAAEVKGIDFTTSPNRSPNGQFASSFIGLA	201
Sbjct 61	SQPNLKQVSFGAKGNIGITYANMMSIKKELE AAEVKGIDFTTSPNRSPNGQFASSFIGLA	120
Query 202	QLHENEDGSKSLLGTSGMESSLNSILAGTDGIITYEKDRGNIVPGTEQVSQRTMDGKD	261
Sbjct 121	QLHENEDGSKSLLGTSGMESSLNSILAGTDGIITYEKDRGNIVPGTEQVSQQTVDGKD	180
Query 262	YTTISSLQSFMETQMDAFQEKVKGKYMATAVLVSAKTGEILATTQRPTFDADTKEGITED	321
Sbjct 181	YTTISSLQSFMETQMDAF +KVVKGKYMATAVLVSAKTGEILATTQRPTF+ADTKEGITED	240
Query 322	FVWRDILYQSNYEPGSTMVKVMMIAAAIDNNTFPGGEVFNSSELKIADATIRWDVNNEG	381
Sbjct 241	FVWRDILYQSNYEPGS +KVM LA++IDNNTFP GE FNSSE KIAD T RDWDVN+GLT	300
Query 382	GGRMMTFSQGFAHSSNVGM+LLEQKMGDATWLDPYKFGVPTRFGLTDEYAGQLPADN	441
Sbjct 301	TGGMMTFLQGFAHSSNVGMSLLEQKMGDATWLDPYKFGVPTRFGLTDEYAGQLPADN	360
Query 442	IVNIAQSSFGQGIVSQTQTMIRFTAIAANDGVMLEPKFISAIYDPNDQTARKSQKEIVGN	501
Sbjct 361	IVNIAQSSFGQGIVSQTQTM+RA TAIANDGVMLEPKFISAIYD N+Q+ RKSQKEIVG	420
Query 502	PVSKDAASLTRTNMVLVGTDPPVYGTMYNHSTGKPTVTVPQNVALKSGTAQIADEKNGGY	561
Sbjct 421	PVSEDAASLTRTNMILVGTDPYKFGVPTRFGLTDEYAGQLPADN	480
Query 562	LVLGTDYIFSAVSMSPAENPDFILYVTVQQPEHYSIGIQLGEFANPILERASAMKDSLNLQ	621
Sbjct 481	LVLG T +YIFS V +M+PAENPDFILYVTVQQPEHYSIGIQLGEFA PILERASAMK+SLNLQ	540
Query 622	TTAKALEQVSSQSPYPMPSVKDISPGDLAEELRRNLVQPIVVGTGKIKNSSAEEGKNLA	681
Sbjct 541	TTAKALEQVSSQSPYPMPSVKDISPGDLAEELRRNLVQPIVVGTGKIKNSSAEEGKNLA	600
Query 682	PNQQVLILSDKAEEVPDMYGWTKETAETLAKWLNLIELEFQGSGSTVQKQDVRANTAIKDI	741
Sbjct 601	PNQQVLILSDKAEEVPDMYGWTKETAETLAKWLNLIELEFQGSGSTVQKQDVRANTAIKDI	660
Query 742	KKITLTLGD 750	
Sbjct 661	KKITLTLGD 669	

>gb|AY56850.1| penicillin-binding protein 2X [Streptococcus pneumoniae]
 Length=670

Score = 1206 bits (3119), Expect = 0.0, Method: Composition-based stats.
 Identities = 627/670 (93%), Positives = 647/670 (96%), Gaps = 0/670 (0%)

Query 81	DRNGVPIAEDATSYNVYAVIDENYKSATGKILYVEKTQFNKVAEVFKYLDMEESYVREQ	140
Sbjct 1	DRNGVPIAEDATSYNVYAVIDENYKSATGKILYVEKTQFNKVAEVFKYLDMEESYVREQ	60
Query 141	LSQPNLKQVSFGAKGNIGITYANMMSIKKELEAAEVKGIDFTTSPNRSPNGQFASSFIGL	200
Sbjct 61	LSQPNLKQVSFGAKGNIGITYANMMSIKKELE AEVKGIDFTTSPNRSPNGQFASSFIGL	120
Query 201	AQLHENEDGSKSLLGTSGMESSLNSILAGTDGIITYEKDRGNIVPGTEQVSQRTMDGKD	260
Sbjct 121	AQLHENEDGSKSLLGTSGMESSLNSILAGTDGIITYEKDRGNIVPGTEQVSQQTVDGKD	180
Query 261	VYTTISSLQSFMETQMDAFQEKVKGKYMATAVLVSAKTGEILATTQRPTFDADTKEGITE	320
Sbjct 181	VYTTISSLQSFMETQMDAFLEVKVKGKYMATAVLVSAKTGEILATTQRPTFNADTKEGITE	240

Query	321	DFVWRDILYQSNYEPGSTMVKVMMIAAAIDNNTFPGGEVFNSSELKIAADATIRDWDVNNEGL	380
Sbjct	241	DFVWRDILYQSNYEPGS MKVM LA++IDNNTFP GE FNSSE KIADAT RDWDVN+GL	300
Query	381	TGGRMMTFSQGFAHSSNVGMLLEQKMGDATWLDYLNRFKFGVPTRFGLTDEYAGQLPAD	440
Sbjct	301	TTGGMMTFLQGFAHSSNVGMSLLEQKMGDATWLDYLKRKFGVPTRFGLTDEYAGQLPAD	360
Query	441	NIVNIAQSSFGQGISVTQTQMIRAFTAIANDGVMLEPKFISAIYDPNDQTARKSQKEIVG	500
Sbjct	361	NIVSIAQSSFGQGISVTQTQM+RAFTAIANDGVMLEPKFISAIYD N+Q+ RKSQKEIVG	420
Query	501	NPVSKDAASLTRTNMVLVGTDPVYGTMYNHSTGKPTTVPGQNVALKSGTAQIADEKNGG	560
Sbjct	421	NPVSK+AAS TR +M+LVGTDP+YGTMYNH TGKP +TVPGQNVKA+KSGTAQIADEKNGG	480
Query	561	YLVGLTDYIFSAVSMSPAENPDFILYVTVQQPEHYSGIQLGEFANPILERASAMKDSLNL	620
Sbjct	481	YLVGSTNYIFSVVTMNPAENPDFILYVTVQQPEHYSGIQLGEFATPILERASAMKDSLNL	540
Query	621	QTTAKALEQVSQQSPYPPMSVKDISPGDLAELRRNLVQPIVVGTGKIKNSSAEEGKNL	680
Sbjct	541	QTTAKALEQVSQQSPYPPMSVKDISPGDLAELRRNLVQPIVVGTGKIKNSSAEEGKNL	600
Query	681	APNQQLILSDKAAEVPDMDYGTWTKETAETLAKWLNLIEFQGSGSTVQKQDVRANTAIKD	740
Sbjct	601	APNQQLILSDK EEVPDMDYGTWTKETAETLAKWLNLIEFQGSGSTVQKQDVRANTAIKD	660
Query	741	IKKITLTLD 750	
Sbjct	661	IKKITLTLD 670	

>gb|AY56847.1| penicillin-binding protein 2X [Streptococcus pneumoniae]
Length=669

Score = 1204 bits (3114), Expect = 0.0, Method: Composition-based stats.
Identities = 621/669 (92%), Positives = 644/669 (96%), Gaps = 0/669 (0%)

Query	82	RNGVPIAEDATSYNVYAVIDENYKSATGKILYVEKTQFNKVAEVFKYLDMEESYVREQL	141
Sbjct	1	RNGVPIAEDATSYNVYAVIDENYKSATGKILYVEKTQFNKVAEVFKYLDMEESYVREQL	60
Query	142	SQPNLKQVSFGAKGNIGITYANMMSIKKELEAAEVKGIDFTTSPNRSPNGQFASSFIGLA	201
Sbjct	61	SQPNLKQVSFGAKGNIGITYANMMSIKKELEAAEVKGIDFTTSPNRSPNGQFASSFIGLA	120
Query	202	QLHENEDGSKSLLGTSGMESSLNSILAGTDGIITYEKDRLGNIVPGTEQVSQRTMDGKDV	261
Sbjct	121	QLHENEDGSKSLLGTSGMESSLNSILAGTDGIITYEKDRLGNIVPGTEQVSQRTMDGKDV	180
Query	262	YTTISSPLQSFMETQMDAQEKKVKGKYMTATLVSAKTGEILATTQRPTFDADTKEGITED	321
Sbjct	181	YTTISSPLQSFMETQMDAQEKKVKGKYMTATLVSAKTGEILATTQRPTFDADTKEGITED	240
Query	322	FVWRDILYQSNYEPGSTMVKMIAAAIDNNTFPGGEVFNSSELKIAADATIRDWDVNNEGLT	381
Sbjct	241	FVWRDILYQSNYEPGSTMVKMIAAAIDNNTFPGGEVFNSSELKIAADATIRDWDVNNEGLT	300
Query	382	GGRMMTFSQGFAHSSNVGMLLEQKMGDATWLDYLNRFKFGVPTRFGLTDEYAGQLPADN	441
Sbjct	301	GGRMMTFSQGFAHSSNVGMLLEQKMGDATWLDYLNRFKFGVPTRFGLTDEYAGQLPADN	360
Query	442	IVNIAQSSFGQGISVTQTQMIRAFTAIANDGVMLEPKFISAIYDPNDQTARKSQKEIVGN	501
Sbjct	361	IVNIA S+FGQGISVTQTQM+RAFTAIANDGVMLEPKFISA+YDPNDQ+ RKSQKE+VGN	420
Query	502	PVSKDAASLTRTNMVLVGTDPVYGTMYNHSTGKPTTVPGQNVALKSGTAQIADEKNGGY	561
Sbjct	421	PVSKDAASVTRDQMVMVGTDPYGTMYNHSTGKATVNPVPGQNVALKSGTAQIADEKNGGY	480
Query	562	LVGLTDYIFSAVSMSPAENPDFILYVTVQQPEHYSGIQLGEFANPILERASAMKDSLNLQ	621
Sbjct	481	LVGLTDYIFSAVSMSPAENPDFILYVTVQQPEHYSGIQLGEFANPILERASAMKDSLNLQ	540
Query	622	TTAKALEQVSQQSPYPPMSVKDISPGDLAELRRNLVQPIVVGTGKIKNSSAEEGKNLAA	681
Sbjct	541	TTAKALEQVSQQSPYPPMSVKDISPGDLAELRRNLVQPIVVGTGKIKNSSAEEGKNLAA	600
Query	682	PNQQVLILSDKAAEVPDMDYGTWTKETAETLAKWLNLIEFQGSGSTVQKQDVRANTAIKDI	741
Sbjct	601	PNQQVLILSDK EEVPDMDYGTWTKETAETLAKWLNLIEFQGSGSTVQKQDVRNTAIKNI	660
Query	742	KKITLTLD 750	
		KKI LTLD	

- Sbjct 661 KKIKLTLGD 669

>gb|AYY56846.1| penicillin-binding protein 2X [Streptococcus pneumoniae]
Length=670

Score = 1198 bits (3099), Expect = 0.0, Method: Composition-based stats.
Identities = 621/670 (92%), Positives = 647/670 (96%), Gaps = 0/670 (0%)

Query	81	DRNGVPIAEDATSYNVAVIDENYSATGKILYVEKTQFNKVAEVFKYLDMEESYVREQ	140
Sbjct	1	DRNGVPIAEDATSYNVAVIDENYSATGKILYVEKTQFNKVAEVFKYLDMEESYVREQ	60
Query	141	LSQPNLKQVSFGAKGNIGITYANMMSIKKELEAAEVKGIDFTTSPNRSPNGQFASSFIGL	200
Sbjct	61	LSQPNLKQVSFGAKGNIGITYANMM+IKKELE AEVKGIDFTTSPNRSPNGQFASSFIGL	120
Query	201	AQLHENEDGSKSLLGTSGMESSLNSILAGTDGIITYEKDRLGNIVPGTEQVSQRTMDGKD	260
Sbjct	121	AQLHENEDGSKSLLGTSGMESSLNSILAGTDGIITYEKDRLGNIVPGTEQVSQQTVDGKD	180
Query	261	VYTTISSLQSFMETQMDFQEKVKGKYMATAVLVSAKTCGEILATTQRPTFDADTKEGITE	320
Sbjct	181	VYTTISSLQSFMETQMDFQEKVKGKYMATAVLVSAKTCGEILATTQRPTFDADTKEG+T+	240
Query	321	DFVWRDILYQSNYEPGSTMKVMMLAAAIDNNTFPGGEVFNSSELKIAADATIRWDVNNEGL	380
Sbjct	241	DFVWRDILYQSNYEPGSTMKVMMLAAAIDNNTFPGGEVFNSSELK+AD TIRWDVNNEGL	300
Query	381	TGGRMMTFSQGFAHSSNVGMTLLEQKMGDATWLDYLNRFKFGVPTRFGLTDEYAGQLPAD	440
Sbjct	301	TGGGMMTFSQGFAHSSNVGMTLLEQKMGDATWLDYLNRFKFGVPTRFGLTDEYAGQLPAD	360
Query	441	NIVNIAQSSFGQGISVTQTQMIRAFTAIANDGVMLEPKFISAIYDPNDQTARKSQKEIVG	500
Sbjct	361	NIVNIAQSSFGQGISVTQTQMIRAFTAIANDGVMLEPKFISAIYDPNDQSVRKSQKEIVG	420
Query	501	NPVSKDAASLRTNMVLVGTDPVYGTMYNHSTGKPTVTPGQNVALKSGTAQIADEKNGG	560
Sbjct	421	NPVSK+AAS+TR +MV+VGTDP YGTMYNHSTGKPTVTPGQNVALKSGTA+IADEKNGG	480
Query	561	YLVGLTDYIFSAVSMSPAENPDFILYVTVQQPEHYSGIQLGEFANPILERASAMKDSLNL	620
Sbjct	481	YLVGLTDYIFSAVSM+PAENPDFILYVTVQQPEHYSGIQLGEFANPILERASAMK+SLNL	540
Query	621	QTTAKALEQVSQQSPYPMPSVKDISPGDLAEEELRRNLVQPIVVGTGKIKNNSAEEGKNL	680
Sbjct	541	QTTAKALEQFSKTTSYAMPATKDYPGDLAEEELRRNLVQPIVVGTGKIKETSVEEGTNL	600
Query	681	APNQQVLILSDKAEEVPDMYGTWTKETAETLAKWLNIIEFQGSGSTVQKQDVRANTAIKD	740
Sbjct	601	APNQQVL+LSDK EE+PDMDYGW KETAET AKWLNIIEF+GSGSTVQKQDVRANTAIKD	660
Query	741	IKKITLTLGD 750	
Sbjct	661	IKKITLTLGD 670	

>gb|AYY56857.1| penicillin-binding protein 2X [Streptococcus pneumoniae]
Length=666

Score = 1197 bits (3096), Expect = 0.0, Method: Composition-based stats.
Identities = 623/666 (93%), Positives = 643/666 (96%), Gaps = 0/666 (0%)

Query	85	VPIAEDATSYNVAVIDENYSATGKILYVEKTQFNKVAEVFKYLDMEESYVREQLSQP	144
Sbjct	1	VPIAEDATSYNVAVIDENYSATGKILYVEKTQFNKVAEVFKYLDMEESYVREQLSQP	60
Query	145	NLKQVSFGAKGNIGITYANMMSIKKELEAAEVKGIDFTTSPNRSPNGQFASSFIGLAQLH	204
Sbjct	61	NLKQVSFGAKGNIGITYANMMSIKKELE AEVKGIDFTTSPNRSPNGQFASSFIGLAQLH	120
Query	205	ENEDGSKSLLGTSGMESSLNSILAGTDGIITYEKDRLGNIVPGTEQVSQRTMDGKDVT	264
Sbjct	121	ENEDGSKSLLGTSGMESSLNSILAGTDGIITYEKDRLGNIVPGTEQVSQQTVDGKDVT	180
Query	265	ISSPLQSFMETQMDAFQEKVKGKYMATAVLVSAKTCGEILATTQRPTFDADTKEGITEDFW	324
Sbjct	181	ISSPLQSFMETQMDAF EKVKGKYMATAVLVSAKTCGEILATTQRPTF+ADTKEGITEDFW	240
Query	325	RDILYQSNYEPGSTMKVMMLAAAIDNNTFPGGEVFNSSELKIAADATIRWDVNNEGLTGG	384
Sbjct	241	RDILYQSNYEPGSAMKVMTLASSIDNNTFPSGEYFNNSSEFKIADATTRWDVNNDGLTTGG	300
Query	385	MMTFSQGFAHSSNVGMTLLEQKMGDATWLDYLNRFKFGVPTRFGLTDEYAGQLPADNIV	444
		MMTF QGFAHSSNVGM+LLEQKMGDATWLDYL RFKFGVPTRFGLTDEYAGQLPADNIV+	

- Sbjct	301	MMTFLQGFAHSSNVGMSLLEQKMGDATWLDYLRKFKGVPTRFGLTDEYAGQLPADNIVS	360
Query	445	IAQSSFGQGQISVTQTQMIRAFTAIANDGVMLEPKFISAIYDPNDQTARKSQKEIVGNPVS	504
- Sbjct	361	IAQSSFGQGQISVTQTQMLRAFTAIANDGVMLEPKFISAIYDTNNQSVRKSQKEIVGNPVS	420
Query	505	KDAASLTTRTNMVLVGTDPVYGTMYNHSTGKPTVTVPQONVALKSGTAQIADEKNNGYLVG	564
Sbjct	421	K+AAS TR +M+LVGTD+YGTMYNH TGKP +TVPGQNV+A+KSGTAQIADEKNNGYLVG	480
Query	565	KEAASSTTRNHLILVGTDPLYGTMYNHGTGPIITVPGQNVAVKSGTAQIADEKNNGYLVG	624
Sbjct	481	STNYIIFSVVTTMNPAENPDFILYVTVQQPEHYSGIQLGEFATPILERASAMKDSLNLQTTA	540
Query	625	KALEQVSSQQSPYPMPSVKDISPGDLAEELRRNLVQPIIVVGTGKIKKNSSAEEGKNLAPNQ	684
Sbjct	541	KALEQVSSQQSPYPMPSVKDISPGDLAEELRRNLVQPIIVVGTGKIKKNSSAEEGKNLAPNQ	600
Query	685	QLLILSDKAAEVPDMYGTWTKETAETLAKWLNLIELEFQGSGSTVQKQDVRANTAIKDIKKI	744
Sbjct	601	QLLILSDK EEVVPDMYGTWTKETAETLAKWLNLIELEFQGSGSTVQKQDVRANTAIKDIKKI	660
Query	745	TTLGD 750	
Sbjct	661	TTLGD 666	

>emb|CAB65444.1| penicillin binding protein 2x [Streptococcus pneumoniae]
Length=666

Score = 1188 bits (3073), Expect = 0.0, Method: Composition-based stats.
Identities = 612/666 (91%), Positives = 640/666 (96%), Gaps = 0/666 (0%)

Query	85	VPIAEDATSYNVYAVIDENYKSATGKILYVEKTQFNKVAEVFKYLDMEESYVREQLSQP	144
Sbjct	1	VPIAEDATSYNVYAVIDENYKSATGKILYVEKTQFNKVAEVFKYLDMEESYVREQLSQP	60
Query	145	NLKQVSFGAKGNGITYANMMSIKKELEAAEVKGIDFTTSPNRSPNGQFASSFIGLAQLH	204
Sbjct	61	NLKQVSFGAKGNGITYANMMSIKKELEAAEVKGIDFTTSPNRSPNGQFASSFIGLAQLH	120
Query	205	ENEDGSKSLLGTSGMESSLNSILAGTDGIITYEKDRLGNIVPGTEQVSQRTMDGKDVTYTT	264
Sbjct	121	ENEDGSKSLLGTSGMESSLNSILAGTDGIITYEKDRLGNIVPGTEQVSQQTVDGKDVTYTT	180
Query	265	ISSPLQSFMETQMDAFQEKVKGKYMATTLSAKTGEILATTQRPTFDADTKEGITEDFWW	324
Sbjct	181	+SSPLQSFMETQMDAF +KVKGKYMATTLSAKTGEILATTQRPTF+ADTKEGITEDFWW	240
Query	325	RDILYQSNYEPGSTMVKVMMLAAAIDDNNTFPGEVFNSSELKIADATIRDWDVNNEGLTGGR	384
Sbjct	241	MKVM LAAAIDDNNTFPGE FNSSELKIAD TIRDWDVN+GLT GR	300
Query	385	MMTFSQGFAHSSNVGMLLEQKMGDATWLDYLNRFKGVPTRFGLTDEYAGQLPADNIVN	444
Sbjct	301	MMTF QGFA SSNVGM+LLEQKMGD TWLDYLNRFKGVPTRFGLTDEYAGQLPADNIVN	360
Query	445	IAQSSFGQGQISVTQTQMIRAFTAIANDGVMLEPKFISAIYDPNDQTARKSQKEIVGNPVS	504
Sbjct	361	IAQSSFGQGQISVTQTQMIRAFTAIANDGVMLEPKFISAIYDPNDQTVRKSQKEIVGNPVS	420
Query	505	KDAASLTTRTNMVLVGTDPVYGTMYNHSTGKPTVTVPQONVALKSGTAQIADEKNNGYLVG	564
Sbjct	421	KDAASLTTRTNM+LVGTD+YGTMYNH STGKPTVTVPQONVALKSGTA+IADEKNNGYLVG	480
Query	565	LTDYIIFSAVSMSPAENPDFILYVTVQQPEHYSGIQLGEFANPILERASAMKDSLNLQTTA	624
Sbjct	481	T+YIFS V+M+PAENPDFILYVTVQQPEHYSGIQLGEFANPILERASAMK+SLNLQ+ A	540
Query	625	STNYIIFSVVAMNPAENPDFILYVTVQQPEHYSGIQLGEFANPILERASAMKESLNLQSPA	
Sbjct	541	KALEQVSSQQSPYPMPSVKDISPGDLAEELRRNLVQPIIVVGTGKIKKNSSAEEGKNLAPNQ	684
Query	685	KNLQDQVTTESSYAMPSIKDISPGELAETLRRNIVQPIIVVGTGKIKETSVEEGKNLAPNQ	600
Sbjct	601	QLLILSDK VEEIPDMYGWK KETAETFAKWL+IELEF+GSGS VQKQDVR NTAIK+IKKI	660
Query	745	TTLGD 750	
Sbjct	661	LTLGD 666	

>gb|AAN32852.1| penicillin-binding protein 2X [Streptococcus pneumoniae]
gb|AAN32853.1| penicillin-binding protein 2X [Streptococcus pneumoniae]
gb|AAN32854.1| penicillin-binding protein 2X [Streptococcus pneumoniae]
Length=661

		Score = 1187 bits (3071), Expect = 0.0, Method: Composition-based stats.
		Identities = 618/661 (93%), Positives = 638/661 (96%), Gaps = 0/661 (0%)
Query 90	DATSYNVYAVIDENYSATGKILYVEKTQFNKVAEVFKYLDMEESYVREQLSQPNLKQV	149
Sbjct 1	DATSYNVYAVIDENYSATGKILYVEKTQFNKVAEVFKYLDMEESYVREQLSQPNLKQV	60
Query 150	SFGAKGNIGINANMMSIKKELEAAEVKGIDFTTSPNRSPNGQFASSFIGLAQLHENEDG	209
Sbjct 61	SFGAKGNIGINANMMSIKKELEAEVKGIDFTTSPNRSPNGQFASSFIGLAQLHENEDG	120
Query 210	SKSLLGTSGMESSLNSILAGTDGIITYEKDRLGNIVPGTEQVSQRTMDGKDVTYTTISPL	269
Sbjct 121	SKSLLGTSGMESSLNSILAGTDGIITYEKDRLGNIVPGTEQVSQQTVDGKDVTYTTISSTL	180
Query 270	QSFMETQMDAFQEVKVGKYMATTLSAKTGEILATTQRPTFDADTKEGITEDFVWRDILY	329
Sbjct 181	QSFMETQMDAF EKVKGKYMATTLSAKTGEILATTQRPTF+ADTKEGITEDFVWRDILY	240
Query 330	QSNYEPGSTMVKVMMALAAIDNNTFPGEVFNSSELKIADATIRDWDVNNEGLTGGRMMTFS	389
Sbjct 241	QSNYEPGS MKVM LA++IDNNTFP GE FNSSE KIADAT RDWDVN+GLT G MMTF	300
Query 390	QGFAHSSNVGMTLLEQKMGDATWLDYLNRFKFGVPTRFGLTDEYAGQLPADNIVNIAQSS	449
Sbjct 301	QGFAHSSNVGM+LLEQKMGDATWLDYL RFKFGVPTRFGLTDEYAGQLPADNIV+IAQSS	360
Query 450	FGQQGISVTQTQMIRAFATAIANDGVMLEPKFISAIYDPNDQTARKSQQKEIVGNPVSCKAAS	509
Sbjct 361	FGQQGISVTQTQM+RAFTAIA ANDGVMLEPKFISAIYD N+Q+ RKSQKEIVGNPVSCK+AAS	420
Query 510	LTRTNMVLVGTDPVYGTMYNHSTGKPTVTVPQONVALSGTAQIADEKNGGYLVGLTDYI	569
Sbjct 421	TR +M+LVGTD+YGTMYNH TGKP +TVPGQNV+KSGTAQIADEKNGGYLVG T+YI	480
Query 570	FSAVSMSPAENPDFILYVTVQOPEHYSGIQLGEFANPILERASAMKDSLNLQTTAKALEQ	629
Sbjct 481	FSVVTMNPAENPDFILYVTVQOPEHYSGIQLGEFA PILERASAMKDSLNLQTTAKALEQ	540
Query 630	VSQQSPYPMPSVKDISPGDLAEELRRNLVQPIIVVGTGTKIKNSSAEEGKNLAPNQVLIL	689
Sbjct 541	VSQQSPYPMPSVKDISPGDLAEELRRNLVQPIIVVGTGTKIKNSSAEEGKNLAPNQVLIL	600
Query 690	SDKAEEVPDMYGTWTKETAETLAKWLNLIELEFQGSGSTVQKQDVRANTAIKDIKKITLTG	749
Sbjct 601	SDK EEVVPDMYGTWTKETAETLAKWLNLIELEFQGSGSTVQKQDVRANTAIKDIKKITLTG	660
Query 750	D 750	
Sbjct 661	D 661	

>gb|AAN32861.1| penicillin-binding protein 2X [Streptococcus pneumoniae]
Length=661

	Score = 1186 bits (3069), Expect = 0.0, Method: Composition-based stats.
	Identities = 614/661 (92%), Positives = 635/661 (96%), Gaps = 0/661 (0%)
Query 90	DATSYNVYAVIDENYSATGKILYVEKTQFNKVAEVFKYLDMEESYVREQLSQPNLKQV
Sbjct 1	DATSYNVYAVIDENYSATGKILYVEKTQFNKVAEVFKYLDMEESYVREQLSQPNLKQV
Query 150	SFGAKGNIGINANMMSIKKELEAAEVKGIDFTTSPNRSPNGQFASSFIGLAQLHENEDG
Sbjct 61	SFGAKGNIGINANMMSIKKELEAEVKGIDFTTSPNRSPNGQFASSFIGLAQLHENEDG
Query 210	SKSLLGTSGMESSLNSILAGTDGIITYEKDRLGNIVPGTEQVSQRTMDGKDVTYTTISPL
Sbjct 121	SKSLLGTSGMESSLNSILAGTDGIITYEKDRLGNIVPGTEQVSQQTVDGKDVTYTTISSTL
Query 270	QSFMETQMDAFQEVKVGKYMATTLSAKTGEILATTQRPTFDADTKEGITEDFVWRDILY
Sbjct 181	QSFMETQMDAF+AFQEVKVGKYMATA LVSAKTGEILATTQRPTFDADTKEG+T+DFVWRDILY
Query 330	QSNYEPGSTMVKVMMALAAIDNNTFPGEVFNSSELKIADATIRDWDVNNEGLTGGRMMTFS
Sbjct 241	QSNYEPGS MKVM LAAAIDNNTFPGEVFNSSELK+AD TIRDWDVNNEGLTGG MMTFS
Query 390	QGFAHSSNVGMTLLEQKMGDATWLDYLNRFKFGVPTRFGLTDEYAGQLPADNIVNIAQSS
Sbjct 301	QGFAHSSNVGM+LLEQKMGDATWLDYL RFKFGVPTRFGLTDEYAGQLPADNIV+IAQSS
Query 450	FGQQGISVTQTQMIRAFATAIANDGVMLEPKFISAIYDPNDQTARKSQQKEIVGNPVSCKAAS
Sbjct 361	FGQQGISVTQTQM+RAFTAIA ANDGVMLEPKFISA+YDPNDQT RKSQKEIVGNPVSCKAAS

Query	510	LTRTNMVLVGTDPVYGTMYNHSTGKPTVTVPQNVALKSGTAQIADEKNGGYLVGLTDYI	569
		TRT+MVLVGTDPVYGT+NHSTGKPTVTVPQNVALKSGTAQIADEKNGGYLVG TDYI	
Sbjct	421	QTRTHMVLVGTDPVYGTMHNSTGKPTVTVPQNVALKSGTAQIADEKNGGYLVGTTDYI	480
Query	570	FSAVSMSPAENPDFILYVTVQQPEHYSGIQLGEFANPILERASAMKDSLNLQTTAKALEQ	629
		FSAVSM+PAENPDFILYVTVQQPEHYSGIQLGEFANPILERAMKDSLNLQ+TAK L+Q	
Sbjct	481	FSAVSMNPAENPDFILYVTVQQPEHYSGIQLGEFANPILERAVAMKDSLNLQSTAKLDQ	540
Query	630	VQQSPYPMPSVKDISPGDLAEEELRRNLVQPIVVGTGKIKNSAAEGKNLAPNQQVLIL	689
		V+ QS Y MPS+KDISPGDLAE LRRN+VQPIVVGTGKIK SS EEG NLAPNQQV++L	
Sbjct	541	VTNQSAYAMPSIKDISPGDLAEALRRNIVQPIVVGTGKIKESSVEEGTNLAPNQQVILL	600
Query	690	SDKAEEVPDMYGTWTKETAETLAKWLNLIELEFQGSGSTVQKQDVRANTAIKDIKKITLTG	749
		SDK EE+PDMYGW KETAET AKWL+IELEF+GSGS VQKQDVR NTAIK+IKKI LTG	
Sbjct	601	SDKVEEIPDMYGWKETAETFAKWL DIELEFEGSGSVVQKQDVRTNTAIKNIKKIKLTG	660
Query	750	D 750	
		D	
Sbjct	661	D 661	

>gb|AAN32863.1| penicillin-binding protein 2X [Streptococcus pneumoniae]
Length=661

Score = 1183 bits (3061), Expect = 0.0, Method: Composition-based stats.
Identities = 611/661 (92%), Positives = 639/661 (96%), Gaps = 0/661 (0%)

Query	90	DATSYNVAVIDENYSATGKILYVEKTQFNKVAEVFKYLDMEESYVREQLSQPNLKQV	149
		DATSYNVAVIDENYSATGKILYVEKTQFNKVAEVFKYLDMEESYVREQLSQPNLKQV	
Sbjct	1	DATSYNVAVIDENYSATGKILYVEKTQFNKVAEVFKYLDMEESYVREQLSQPNLKQV	60
Query	150	SFGAKGNITYANMMSIKKELEAAEVKGIDFTTSPNRSYPNGQFASSFIGLAQLHENEDG	209
		SFG+KGNITYANMMSIKKELE AEVKGIDFTTSPNRSYPNGQFASSFIGLAQLHENEDG	
Sbjct	61	SFGSKGNITYANMMSIKKELEAAEVKGIDFTTSPNRSYPNGQFASSFIGLAQLHENEDG	120
Query	210	SKSLLGTSGMESSLNSILAGTDGIITYEKDRLGNIVPGTEQVSQRTMDGKDVTYTISSPL	269
		SKSLLGTSGMESSLNSILAGTDGIITYEKDRLGNIVPGTEQVSQ+T+DGKDVTYTISSPL	
Sbjct	121	SKSLLGTSGMESSLNSILAGTDGIITYEKDRLGNIVPGTEQVSQQTVDGKDVTYTISSPL	180
Query	270	QSFMETQMDAFQEVKVGKYMATTLSAKTGEILATTQRPTFDADTKEGITEDFVWRDILY	329
		QSFMETQM+AFQEVKVGKYMATTLSAKTGEILATTQRPTFDADTKEG+T+DFVWRDILY	
Sbjct	181	QSFMETQMDAFQEVKVGKYMATTLSAKTGEILATTQRPTFDADTKEGLTKDFVWRDILY	240
Query	330	QSNYEPGSTMKVMMLAAAIDNNTFPGGEVFNSSELKIADATIRWDVNNEGLTGGRMMTFS	389
		QSNYEPGSTMKVM LAAAIDNNTFPGGEVFNSSELKIAD TIRDWDVN+GLT GRMMTF	
Sbjct	241	QSNYEPGSTMKVMTLAAAIDNNTFPGGEVFNSSELKIADVTIRWDVNGLTTGRMMTFL	300
Query	390	QGFAHSSNVGMTLLEQKMGDATWLDYLNRFKFGVPTRFGLTDEYAGQLPADNIVNIAQSS	449
		QGFA SSVGM+LLEQKMGDATWLDYLNRFKFGVPTRFGLTDEYAGQLPADNIVNIAQSS	
Sbjct	301	QGFALSSNVGMSLLEQKMGDATWLDYLNRFKFGVPTRFGLTDEYAGQLPADNIVNIAQSS	360
Query	450	FGQQGISVTQTQMIRAFTAIANDGVMLEPKFISAIYDPNDQTARKSQKEIVGNPVSKDAAS	509
		FGQQGISVTQTQMIRAFTAIANDGVMLEPKFISAIYDPNDQTARKSQKE+VGNPVSKDAAS	
Sbjct	361	FGQQGISVTQTQMLRAFTAIANDGVMLEPKFISAIYDPNDQTARKSQKEVVGVPNSKDAAS	420
Query	510	LTRTNMVLVGTDPVYGTMYNHSTGKPTVTVPQNVALKSGTAQIADEKNGGYLVGLTDYI	569
		LTRTNM+LVGTDPVYGTMYNHSTGKPTVTVPQNVALKSGTAQIADEKNGGYLVGLT+YI	
Sbjct	421	LTRTNMILVGTDPVYGTMYNHSTGKPTVTVPQNVALKSGTAQIADEKNGGYLVGLTNYI	480
Query	570	FSAVSMSPAENPDFILYVTVQQPEHYSGIQLGEFANPILERASAMKDSLNLQTTAKALEQ	629
		FSAVSM+PAENPDFILYVTVQQPEHYSGIQLGEFA PILERASAMK+SLNLQ+ AK L++	
Sbjct	481	FSAVSMNPAENPDFILYVTVQQPEHYSGIQLGEFATPILERASAMKESLNQSPAKNLDK	540
Query	630	VQQSPYPMPSVKDISPGDLAEEELRRNLVQPIVVGTGKIKNSAAEGKNLAPNQQVLIL	689
		V+ +S Y MPS+KDISPG+LAE LRRN+VQPIVVGTGKIK +S EEG NLAPNQQV+L	
Sbjct	541	VTTESSYAMPSIKDISPGELAEALRRNIVQPIVVGTGKIKETSVEEGTNLAPNQQVLLL	600
Query	690	SDKAEEVPDMYGTWTKETAETLAKWLNLIELEFQGSGSTVQKQDVRANTAIKDIKKITLTG	749
		SDK EE+PDMYGW KETAET AKWL+IELEF+GSGS VQKQDVR NTAIK+IKKI LTG	
Sbjct	601	SDKVEEIPDMYGWKETAETFAKWL DIELEFEGSGSVVQKQDVRTNTAIKNIKKIKLTG	660
Query	750	D 750	
		D	
Sbjct	661	D 661	

> pdb|1K25|A **S** Chain A, Pbp2x From A Highly Penicillin-Resistant Streptococcus pneumoniae Clinical Isolate

> pdb|1K25|B **S** Chain B, Pbp2x From A Highly Penicillin-Resistant Streptococcus pneumoniae Clinical Isolate

> pdb|1K25|C **S** Chain C, Pbp2x From A Highly Penicillin-Resistant Streptococcus pneumoniae Clinical Isolate

pdb|1K25|D S Chain D, Pbp2x From A Highly Penicillin-Resistant Streptococcus pneumoniae Clinical Isolate
Length=685

Score = 1183 bits (3060), Expect = 0.0, Method: Composition-based stats.
Identities = 607/685 (88%), Positives = 646/685 (94%), Gaps = 0/685 (0%)

Query	66	HQTRTRVPAKRGTIYDRNGVPIAEDATSYNVAVIDENYKSATGKILYVEKTQFNKVAEV	125
Sbjct	1	HQITRTVPAKRGTIYDRNGVPIAEDATSYNVAVID+ YKSATGKILYVE QFNKVAEV	60
Query	126	FHKYLDMEESYVREQLSQPNLKQVSFGAKGNIGINANMMMSIKKELEAAEVKGIDFTTSPN	185
Sbjct	61	FHKYLDMEESYVREQLSQPNLKQVSFG+KGNGINITYANMM+IKKELE AEVKGIDFTTSPN	120
Query	186	RSYPNGOFASSFIGLAQLHENEDGSKSLLGTSGMESSLNSILAGTDGIITYEKDRGNIV	245
Sbjct	121	RSYPNGQFASSFIGLAQLHENEDGSKSLLGTSGMESSLNSILAGTDGIITYEKDR+GNIV	180
Query	246	PGTEQVSQRTMDGKDVTYTTISPLQSFMETQMDAFQEVKVKGKYMATTLSVAKTGEILATT	305
Sbjct	181	PGTELVSQQTVDGKDVTYTTISPLQSFMETQMDAF EKVKGKYMATTLSVAKTGEILATT	240
Query	306	QRPTFDADTKEGITEDFVWRDILYQSNSYEPGSTMKVMMIAAIIDNNTFPGEVFNSSELK	365
Sbjct	241	QRPTF+ADTKEGITEDFVWRDILYQSNSYEPGS MKVM LA++IDNNTFP GE FNSSELK	300
Query	366	IADATIRDWDVNEGLTGGRMMTFSQGFAHSSNVGMILLEQKMGDATWLDYLNRFKFGVPT	425
Sbjct	301	IADAT RDWDVNEGLT G MMTF QGFAHSSNVGM+LLEQKMGDATWLDYL RFKFGVPT	360
Query	426	RFGLTDEYAGQLPADMINVIAQSSFGQGISVTQMLRAFTAIANDGVMLEPKFISAIYD	485
Sbjct	361	RFGLTDEYAGQLPADMINVIAQSSFGQGISVTQMLRAFTAIANDGVMLEPKFISAIYD	420
Query	486	PNDQTARKSQEIVGNPVSKDAASLTRTNMVLVGTDPVYGTMYNHSTGKPTVTVPQNVA	545
Sbjct	421	N+Q+ RKSQKEIVGNPVSK+AAS TR +M+LVGTD+YGTMYNH TGKP +TVPGQNVA	480
Query	546	LKSGTAQIADEKNGGYLVGLTDYIFSAVMSPAENPDFILYVTVQQPEHYSIGIQLGEFAN	605
Sbjct	481	+KSGTAQIADEKNGGYLVG T+YIFSAV+M+PAENPDFILYVTVQQPEHYSIGIQLGEFA	540
Query	606	PILERASAMKDSLNLQTTAKALEQVQSQQSPYPMPSVKDISPGDLAEELRRNLVQPIVVGT	665
Sbjct	541	PILERASAMK+SLNLQ+ AK L++V+ +S Y MPS+KDISPG+LAE LRRN+VQPIVVGT	600
Query	666	GTKIKNSSAEEGKNLAPNQQVLILSDKAEEVPDMYGTWTKETAETLAKWLNIIELEFQGSGS	725
Sbjct	601	GTKIK +S EEG NLAPNQQVL+LSDK EE+PDMYGW KETAET AKWL+IELEF+GSGS	660
Query	726	GTKIKETSVEEGTNLAPNQQVLLSDKVEEI PDMYGWKKETAETFAKWL DIELEFEGSGS	660
Sbjct	661	TVQKQDVRANTAIKDIKITLTLGD 750	
		VQKQDVR NTAIK+IKKI LTLGD	
		VVQKQDVRTNTAIKNIKKIKLTLGD 685	

>**gb|ABB46505.1| penicillin binding protein 2x [Streptococcus pneumoniae]**
Length=657

Score = 1182 bits (3059), Expect = 0.0, Method: Composition-based stats.
Identities = 614/657 (93%), Positives = 635/657 (96%), Gaps = 0/657 (0%)

Query	94	YNVYAVIDENYKSATGKILYVEKTQFNKVAEVFKYLDMEESYVREQLSQPNLKQVSFGA	153
Sbjct	1	YNVYAVIDENYKSATGKILYVEKTQFNKVAEVFKYLDMEESYVREQLSQPNLKQVSFGA	60
Query	154	KGNIGINANMMMSIKKELEAAEVKGIDFTTSPNRSPNGQFASSFIGLAQLHENEDGSKSL	213
Sbjct	61	KGNIGINANMMMSIKKELEAAEVKGIDFTTSPNRSPNGQFASSFIGLAQLHENEDGSKSL	120
Query	214	LGTSGMESSLNSILAGTDGIITYEKDRGNIVPGTEQVSQRTMDGKDVTYTTISPLQSFN	273
Sbjct	121	LGTSGMESSLNSILAGTDGIITYEKDRGNIVPGTEQVSQQTVDGKDVTYTTISPLQSFN	180
Query	274	ETQMDAFQEVKKGKYMATTLSVAKTGEILATTQRPTFDADTKEGITEDFVWRDILYQS	333
Sbjct	181	ETQMDAF EKVKGKYMATTLSVAKTGEILATTQRPTF+ADTKEGITEDFVWRDILYQS	240
Query	334	EPGSTMKVMMIAAIIDNNTFPGEVFNSSELKIAADATIRDWDVNEGLTGGRMMTFSQGFA	393
Sbjct	241	EPGS MKVM LA+++DNNTFP GE FNSSE KIADAT RDWDVN+GLT G MMTF QGFA	300
Query	394	HSSNVGMTLLEQKMGDATWLDYLNRFKFGVPTRFGLTDEYAGQLPADMINVIAQSSFGQG	453
Sbjct	301	HSSNVGM+LLEQKMGDATWLDYL RFKFGVPTRFGLTDEYAGQLPADMINVIAQSSFGQG	360

Query	454	ISVTQTCMIRAFATIANDGVMLEPKFISAIYDPNDQTARKSQKEIVGNPVSCKDAASLRT	513
Sbjct	361	ISVTQTCMIRAFATIANDGVMLEPKFISAIYD N+Q+ RKSQKEIVGNPVSCKDAASLRT	420
Query	514	NMVLVGTDPVYGTMYNHNSTGKPTTVPGQNVALKSGTAQIADEKNGGYLVGLTDYIFSAV	573
Sbjct	421	+M+LVGTD+YGTMYNH TGKP +TVPGQNV+A KSGTAQIADEKNGGYLVG T+YIFS V	480
Query	574	SMSPAENPDFILYVTVQQPEHYSGIQLGEFANPILERASAMKDSLNQTTAKALEQVSQQ	633
Sbjct	481	+M+PAENPDFILYVTVQQPEHYSGIQLGEFA PILERASAMKDSLNQTTAKALEQVSQQ	540
Query	634	SPYPMPSVKDISPGDLAEEELRRNLVQPIVVGTTKIKNSSAEGKNLAPNQQVLILSDK	693
Sbjct	541	SPYPMPSVKDISPGDLAEEELRRNLVQPIVVGTTKIKNSSAEGKNLAPNQQVLILSDK	600
Query	694	EEVPDMYGTWTKETAETLAKWLNLIEFQGSGSTVQKQDVRRANTAIKDIKKITLTLGD	750
Sbjct	601	EEVPDMYGTWTKETAETLAKWLNLIEFQGSGSTVQKQDVRRANTAIKDIKKITLTLGD	657

>gb|ABB46506.1| penicillin binding protein 2x [Streptococcus pneumoniae]
Length=657

Score = 1181 bits (3055), Expect = 0.0, Method: Composition-based stats.
Identities = 614/657 (93%), Positives = 634/657 (96%), Gaps = 0/657 (0%)

Query	94	YNYAVIDENYKSATGKILYVEKTQFNKVAEVFKYLDMEESYVREQLSQPNLKQVSFGA	153
Sbjct	1	YNYAVIDENYKSATGKILYVEKTQFNKVAEVFKYLDMEESYVREQLSQPNLKQVSFGA	60
Query	154	KGNIGITYANMMSIKKELEAAEVKGIDFTTSPNRSPNGQFASSFIGLAQLHENEDGSKSL	213
Sbjct	61	KGNIGITYANMMSIKKELEAAEVKGIDFTTSPNRSPNGQFASSFIGLAQLHENEDGSKSL	120
Query	214	LGTSGMESSLNSILAGTDGIITYEKDRGNIVPGTEQVSQRTMDGKDVTISSLQSF	273
Sbjct	121	LGTSGMESSLNSILAGTDGIITYEKDRGNIVPGTEQVSQ+T+DGKDVTISSLQSF	180
Query	274	ETQMDAFQEKVKGKYMATLVSAKTGEILATTQRPTFDADTKEGITEDFVWRDILYQSN	333
Sbjct	181	ETQMDAF EKVKGKYMATLVSAKTGEILATTQRPTF+ADTKEGITEDFVWRDILYQSN	240
Query	334	EPGSTMVKVMMIAAAIDNNTPGGEVFNSSELKIADATIRDWDVNNEGLTGRMMMTFSQGFA	393
Sbjct	241	EPGS MKVM LA++IDNNTFP GE FNSSE KIADAT RDWDVN+GLT G MMTF QGFA	300
Query	394	HSSNVGMTLLEQKMGDATWLDYLNRFKFGVPTRFGLTDEYAGQLPADNIVNIAQSSFGQ	453
Sbjct	301	HSSNVGM+LLEQKMGDATWLDYL RFKFGVPTRFGLTDEYAGQLPADNIV+IAQSSFGQ	360
Query	454	ISVTQTCMIRAFATIANDGVMLEPKFISAIYDPNDQTARKSQKEIVGNPVSCKDAASLRT	513
Sbjct	361	ISVTQTCMIRAFATIANDGVMLEPKFISAIYD N+Q+ RKSQKEIVGNPVSCKDAASLRT	420
Query	514	NMVLVGTDPVYGTMYNHNSTGKPTTVPGQNVALKSGTAQIADEKNGGYLVGLTDYIFSAV	573
Sbjct	421	+M+LVGTD+YGTMYNH TGKP +TVPGQNV+A KSGTAQIADEKNGGYLVG T+YIFS V	480
Query	574	SMSPAENPDFILYVTVQQPEHYSGIQLGEFANPILERASAMKDSLNQTTAKALEQVSQQ	633
Sbjct	481	+M+PAENPDFILYVTVQQPEHYSGIQLGEFA PILERASAMKDSLNQTTAKALEQVSQQ	540
Query	634	SPYPMPSVKDISPGDLAEEELRRNLVQPIVVGTTKIKNSSAEGKNLAPNQQVLILSDK	693
Sbjct	541	SPYPMPSVKDISPGDLAEEELRRNLVQPIVVGTTKIKNSSAEGKNLAPNQQVLILSDK	600
Query	694	EEVPDMYGTWTKETAETLAKWLNLIEFQGSGSTVQKQDVRRANTAIKDIKKITLTLGD	750
Sbjct	601	EEVPDMYGTWTKETAETLAKWLNLIEFQGSGSTVQKQDVRRANTAIKDIKKITLTLGD	657

>gb|AYA56848.1| penicillin-binding protein 2X [Streptococcus pneumoniae]
Length=671

Score = 1180 bits (3052), Expect = 0.0, Method: Composition-based stats.
Identities = 607/671 (90%), Positives = 638/671 (95%), Gaps = 0/671 (0%)

Query	80	YDRNGVPIAEDATSYNVAVIDENYKSATGKILYVEKTQFNKVAEVFKYLDMEESYVRE	139
Sbjct	1	YDRNGVPIAEDATSYNVAVIDENYKSATGKILYVEKTQFNKVAEVFKYLDMEESYVRE	60
Query	140	QLSQPNLKQVSFGAKGNGITYANMMSIKKELEAAEVKGIDFTTSPNRSPNGQFASSFIG	199
Sbjct	61	QLSQPNLKQVSFGAKGNGITYANMMAIKKELEAAEVKGIDFTTSPNRSPNGQFASSFIG	120

Query	200	LAQLHENEDGSKSLLGTSGMESSLNSILAGTDGIITYEKDRLGNIVPGTEQVSQRTMDGK	259
Sbjct	121	LAQLHENEDGSKSLLGTSGMESSLNSILAGTDGIITYEKDR+GNIVPGTE VSQ+T+DGK	180
Query	260	DVYTTISSLPLQSFMETQMDAFQEVKVGKYMATTLSAKTGEILATTQRPTFDADTKEGIT	319
Sbjct	181	DVYTTISSLPLQSFMETQMDAF EKVVGKYMATTLSAKTGEILATTQRPTF+ADTK+GIT	240
Query	320	EDFWRDILYQSNSYEPGSTMKVMMIAAAIDNNTFPGGEVFNSSELKIADATIRDWDVNEG	379
Sbjct	241	+DFWRDILYQSNSYEPGSTMKVMMIAAAIDNNTFPGGE VFNSSELKIADATIRDWDVNEG	300
Query	380	LTGGRMMMTFSQGFAHSSNVGMTLLEQKMGATWLDPYLNRFKFGVPTRFGLTDEYAGQLPA	439
Sbjct	301	LTGGRMMMTFSQGFAHSSNVGMILLEEKMGDTTWLDYLNRFKFGVPTRFGLTDEYAGQLPA	360
Query	440	DNIVNIAQSSFGQGIVTQTQMIRAFTAIANDGVMLEPKFISAIYDPNDQTAKSQKEIV	499
Sbjct	361	DNIVNIAQSSFGQGIVTQTQMIRAFTAIANDGVMLEPKFISAIYDPNDQTAKSQKEIV	420
Query	500	GNPVSKDAASLRTTNMVLVGTDPVYGTMYNHSTGKPTVTVPQONVALKSGTAQIADEKNG	559
Sbjct	421	GNPVSKDAAS TRT MVLVGTDPVYGTMYNHSTGKPTVTVPQONVALKSGTAQIADEKNG	480
Query	560	GYLVGLTDYIIFSAVMSPAENPDFILYVTVQQPEHYSGIQLGEFANPILERASAMKDSL	619
Sbjct	481	GYLVGLTDYIIFSAVMSPAENPDFILYVTVQQPEHYSGIQLGEFANPILERASAMKDSL	540
Query	620	LQTTAKALEQVSSQSPYPMPSVKDISPGDLAEELRRNLVQPIVVGTKIKKNSSAEEGKN	679
Sbjct	541	LQTTAKALEQVSSQSPYPMPSVKDISPGDLAEELRRNLVQPIVVGTKIKKNSSAEEGKN	600
Query	680	LAPNQQVLILSDKAEEVPDMYGTWTKETAETLAKWNLIELEFQGSGSTVQKQDVRNTAIK	739
Sbjct	601	LAPNQQVLILSDKAEEVPDMYGTWTKETAETLAKWNLIELEFQGSGSTVQKQDVRNTAIK	660
Query	740	DIKKITLTLGD 750	
Sbjct	661	NIKKIKLTLGD 671	

>emb|CAB65446.1| penicillin binding protein 2x [Streptococcus pneumoniae]
Length=666

Score = 1179 bits (3051), Expect = 0.0, Method: Composition-based stats.
Identities = 608/666 (91%), Positives = 638/666 (95%), Gaps = 0/666 (0%)

Query	85	VPIAEDATSYNVAVIDENYKSATGKILYVEKTQFNKVAEVFKYLDMEESYVREQLSQP	144
Sbjct	1	VPIAEDATSYNVAVIDENYKSATGKILYVEKTQFNKVAEVFKYLDMEESYVREQLSQP	60
Query	145	NLKQVSFGAKGNGITYANMMSIKKELEAAEVKGIDFTTSPNRSYPNGQFASSFIGLAQLH	204
Sbjct	61	NLKQVSFGAKGNGITYANMMSIKKELEAAEVKGIDFTTSPNRSYPNGQFASSFIGLAQLH	120
Query	205	ENEDGSKSLLGTSGMESSLNSILAGTDGIITYEKDRLGNIVPGTEQVSQRTMDGKDVT	264
Sbjct	121	ENEDGSKSLLGTSGMESSLNSILAGTDGIITYEKDRLGNIVPGTEQVSQRTMDGKDVT	180
Query	265	ISSPLOSFMETQMDAFQEVKVGKYMATTLSAKTGEILATTQRPTFDADTKEGITEDFVW	324
Sbjct	181	ISSPLOSFMETQMDAFQEVKVGKYMATTLSAKTGEILATTQRPTFDADTKEGITEDFVW	240
Query	325	RDILYQSNSYEPGSTMKVMMIAAAIDNNTFPGGEVFNSSELKIADATIRDWDVNEGLTGGR	384
Sbjct	241	RDILYQSNSYEPGSTMKVMMIAAAIDNNTFPGGEVFNSSELKIADATIRDWDVNEGLTGGR	300
Query	385	MMTSQGFAHSSNVGMTLLEQKMGATWLDPYLNRFKFGVPTRFGLTDEYAGQLPADNIVN	444
Sbjct	301	MMTSQGFAHSSNVGMTLLEQKMGATWLDPYLNRFKFGVPTRFGLTDEYAGQLPADNIVN	360
Query	445	IAQSSFGQGIVTQTQMIRAFTAIANDGVMLEPKFISAIYDPNDQTAKSQKEIVGNPVS	504
Sbjct	361	IAQSSFGQGIVTQTQMIRAFTAIANDGVMLEPKFISAIYDPNDQTAKSQKEIVGNPVS	420
Query	505	KDAASLRTTNMVLVGTDPVYGTMYNHSTGKPTVTVPQONVALKSGTAQIADEKNGGYLVG	564
Sbjct	421	KDAASLRTTNMVLVGTDPVYGTMYNHSTGKPTVTVPQONVALKSGTAQIADEKNGGYLVG	480
Query	565	LTDYIIFSAVMSPAENPDFILYVTVQQPEHYSGIQLGEFANPILERASAMKDSLNLQTTA	624
Sbjct	481	T+ IFS V+M+PAENPDFILYVTVQQPEHYSGIQLGEFANPILERASAMKDSLNLQTTA	540
Query	625	KALEQVSQQSPYPMPSVKDISPGDLAEELRRNLVQPIVVGTKIKKNSSAEEGKNLAPNO	684
Sbjct		K L++V+ +S Y MPS+KDISPG+LAE LRRN+VQPIVVGTKIK +S EEG NLAPNO	

Sbjct	541	KNLDKVTESSYAMPSIKDISPGELAEALRRNIVQPIVVGTTKIKETSVEEGTNLAPNQ	600
Query	685	QVLILSDKAAEVPDMYGTWTAKAETLAKWLNLIEFQGSGSTVQKQDVRANTAIKDIKKI QVL+LSDK EE+PDMYGW KETAET AKWL+IELEF+GSGS VQKQDVR NTAIK+IKKI	744
Sbjct	601	QVLLLSDKVEEI PDMYGWKKETAETFAKWL DIELEFEGSGSVVQKQDVRTNTAIKNIKKI	660
Query	745	TTLGD 750 LTLGD	
Sbjct	661	KLTLD 666	

>gb|AAN32859.1| penicillin-binding protein 2X [Streptococcus pneumoniae]
Length=661

Score = 1176 bits (3043), Expect = 0.0, Method: Composition-based stats.
Identities = 606/661 (91%), Positives = 634/661 (95%), Gaps = 0/661 (0%)

Query	90	DATSYNVYAVIDENYKSATGKILYVEKTQFNKVAEVFKYLDMEESYVREQLSQPNLKQV	149
Sbjct	1	DATSYNVYAVIDENYKSATGKILYVEKTQFNKVAEVFKYLDMEESYVREQLSQPNLKQV	60
Query	150	SFGAKGNIGITYANMMSIKKELEAAEVKGIDFTTSPNRSYPNGQFASSFIGLAQLHENEDG	209
Sbjct	61	SFG+KGNGITYANMM+IKKELE AEVKGIDFTTSPNRSYPNGQFASSFIGLAQLHENEDG	120
Query	210	SKSLLGTSGMESSLNSILAGTDGIITYEKDRLGNIVPGTEQVSQ+T+DGKDVTISSL	269
Sbjct	121	SKSLLGTSGMESSLNSILAGTDGIITYEKDRLGNIVPGTEQVSQQTVDGKDVTISSL	180
Query	270	QSFMETQMDAFQEVKVKGKYMATTLSAKTGEILATTQRPTFDADTKEGITEDFVWRDILY	329
Sbjct	181	QSFMETQMDAFQEVKVKGKYMATTLSAKTGEILATTQRPTFDADTKEGITEDFVWRDILY	240
Query	330	QSNYEPGSTMVKVMMAAAIDNNTPGGEVFNSSELKIADATIRWDVNNEGLTGGRMMTFS	389
Sbjct	241	QSNYEPGS MKVMMAAAIDNNTPGGEVFNSSELKIAD TIRWDVNNEGLTGGRMMTFS	300
Query	390	QGFAHSSNVGMTLLEQKMGDATWLDYLNRFKFGVPTRFGLTDEYAGQLPADNIVNIAQSS	449
Sbjct	301	QGFAHSSNVGMTLLEQKMGDATWLDYLNRFKFGVPTRFGLTDEYAGQLPADNIVNIAQSS	360
Query	450	FGQQGISVTQTMIRAFTAIANDGVMLEPKFISAIYDPNDQTARKSQKEIVGNPVSKDAAS	509
Sbjct	361	FGQQGISVTQTMIRAFTAIANDGVMLEPKF+I+A+YDPN+QT R+SQKEIVGNPVSKDAAG	420
Query	510	LTRTNMVLVGTDPVYGTMYNHSTGKPTVTVPGQVALKSGTAQIADEKNGGYLVGLTDYI	569
Sbjct	421	TRT+MVLVGTDP YGTMYNHSTGK TV VPGQVALKSGTA+IADEKNGGYLVG T+ I	
Query	570	QTRTHMVLVGTDPRYGTMYNHSTGKATVNPQVALKSGTAEIADEKNGGYLVGSTNNI	480
Sbjct	481	QTRTHMVLVGTDPRYGTMYNHSTGKATVNPQVALKSGTAEIADEKNGGYLVGSTNNI	
Query	630	QTRTHMVLVGTDPRYGTMYNHSTGKATVNPQVALKSGTAEIADEKNGGYLVGSTNNI	
Sbjct	541	QTRTHMVLVGTDPRYGTMYNHSTGKATVNPQVALKSGTAEIADEKNGGYLVGSTNNI	
Query	690	FSAVSMSPAENPDFILYVTVQOPEHYSGIQLGEFANPILERASAMKDSLNLQTTAKALEQ	629
Sbjct	481	FSAVSMSPAENPDFILYVTVQOPEHYSGIQLGEFANPILERASAMK+SLNLO+ AK L++	
Query	750	FS V+M+PAENPDFILYVTVQOPEHYSGIQLGEFANPILERASAMKESLNQSPAKNLDK	540
Sbjct	661	FSVVAMNPAENPDFILYVTVQOPEHYSGIQLGEFANPILERASAMKESLNQSPAKNLDK	
Query	86	FSVVAMNPAENPDFILYVTVQOPEHYSGIQLGEFANPILERASAMKESLNQSPAKNLDK	
Sbjct	2	FSVVAMNPAENPDFILYVTVQOPEHYSGIQLGEFANPILERASAMKESLNQSPAKNLDK	
Query	146	VQQSPYPMPMSVKDISPGDLAEELRRNLVQPIVVGTTKIKNSSAEEGKNLAPNQQVLIL	689
Sbjct	541	V+ +S Y MPS+KDISPG+LAE LRRN+VQPIVVGTTKIK +S EEG NLAPNQQVL+L	
Query	206	VTTESSYAMPSIKDISPGELAEALRRNIVQPIVVGTTKIKETSVEEGTNLAPNQQVLL	600
Sbjct	122	VTTESSYAMPSIKDISPGELAEALRRNIVQPIVVGTTKIKETSVEEGTNLAPNQQVLL	
Query	266	NEDGSKSLLGTSGMESSLNSILAGTDGIITYEKDRLGNIVPGTEQVSQRTMDGKDVTI	265
Sbjct	122	NEDGSKSLLGTFGLESSLNTILAGTDGIITYEKDRGNIVPGTELVSQQTVDGKDVTI	181
Query	266	SSPLQSFMETQMDAFQEVKVKGKYMATTLSAKTGEILATTQRPTFDADTKEGITEDFVWR	325
Sbjct	661	SSPLQSFMETQMDAF EKVKGKYMATTLSAKTGEILATTQRPTF+ADTK+GIT+DFVWR	

>gb|AYA56854.1| penicillin-binding protein 2X [Streptococcus pneumoniae]
Length=666

Score = 1174 bits (3038), Expect = 0.0, Method: Composition-based stats.
Identities = 607/665 (91%), Positives = 637/665 (95%), Gaps = 0/665 (0%)

Query	86	PIAEDATSYNVYAVIDENYKSATGKILYVEKTQFNKVAEVFKYLDMEESYVREQLSQPN	145
Sbjct	2	PIAEDATSYNVYAVIDENYKSATGKILYVEKTQFNKVAEVFKYLDMEESYVREQLSQPN	61
Query	146	LKQVSFGAKGNIGITYANMMSIKKELEAAEVKGIDFTTSPNRSYPNGQFASSFIGLAQLHE	205
Sbjct	62	LKQVSFGAKGNIGITYANMMSIKKELEAAEVKGIDFTTSPNRSYPNGQFASSFIGLAQLHE	121
Query	206	LKQVSFGAKGNIGITYANMMSIKKELEAAEVKGIDFTTSPNRSYPNGQFASSFIGLAQLHE	
Sbjct	122	NEDGSKSLLGTSGMESSLNSILAGTDGIITYEKDRLGNIVPGTEQVSQRTMDGKDVTI	
Query	266	NEDGSKSLLGTFGLESSLNTILAGTDGIITYEKDRGNIVPGTELVSQQTVDGKDVTI	
Sbjct	122	NEDGSKSLLGTFGLESSLNTILAGTDGIITYEKDRGNIVPGTELVSQQTVDGKDVTI	
Query	266	SSPLQSFMETQMDAFQEVKVKGKYMATTLSAKTGEILATTQRPTFDADTKEGITEDFVWR	325
Sbjct	661	SSPLQSFMETQMDAF EKVKGKYMATTLSAKTGEILATTQRPTF+ADTK+GIT+DFVWR	

Sbjct	182	SSPLQSFMETQMDAFLEKVKKGKYMTATLVSAKTGEILATTQRPTFNADTKDGITKDFVWR	241
Query	326	DILYQSNYEPGSTMVKVMMIAAAIDNNTFPGEVFNSSELKIADATIRDWDVNNEGLTGGRM DILYQ NYEPGS MKVM LA++IDNNTFPGE FNSSE KIAD T RDWDVNNEGLTGG M	385
Sbjct	242	DILYQGNYEPGSAMKVMTLASSIDNNTFPGEYFNSSES KIADVTTRDWDVNNEGLTGGGM	301
Query	386	MTFSQGFAHSSNVGMTLLEQKMGDATWLDYLNRFKFGVPTRFGLTDEYAGQLPADNIVNI MTFSQGFAHSSNVGM LLE+KMGD TWLDYLNRFKFGVPTRFGLTDEYAGQLPADNIVNI	445
Sbjct	302	MTFSQGFAHSSNVGMILLEEKMGDTTWLDYLNRFKFGVPTRFGLTDEYAGQLPADNIVSI	361
Query	446	AQSSFGQGIVSQTQMIRAFTAIANDGVMLEPKFISAIYDPNDQTARKSQKEIVGNPVS K AQSSFGQGIVSQTQMIRAFTAIANDGVMLEPKFI+A+YDPNDQT RKSQKEIVGNPVS K	505
Sbjct	362	AQSSFGQGIVSQTQMIRAFTAIANDGVMLEPKFITALYDPNDQTVRKSQKEIVGNPVS K	421
Query	506	DAASLTTRTNMVLVGTDPVYGTMYNHSTGKPTVTVPQNVALKSGTAQIADEKNGGYLVGL DAAS TRT MVLVGTDPVYGTMYNHSTGKP VTVPQNVALKSGTAQIADEKNGGYLVG	565
Sbjct	422	DAASQTRTQMVLVGTDPVYGTMYNHSTGKPIVTVPQNVALKSGTAQIADEKNGGYLVGP	481
Query	566	TDYIFSAVSMSPAENPDFILYVTVQQPEHYSGIQLGEFANPILERASAMKDSLNLQTTAK T+YIFS V+M+PAENPDFILYVTVQQPEH+SGIQLGEFANPILERASAMK+SLNLQ+ AK	625
Sbjct	482	TNYIFSVVAMNPAENPDFILYVTVQQPEHFSGIQLGEFANPILERASAMKESLNLQSPAK	541
Query	626	ALEQVSQQSPYPMPSVKDISPGDLAEEELRRNLVQPIVVGTTKIKNSSAEKGKNLAPNQQ L+QV+ +S Y MPS+KDISPG+LAE LRRN+VQPIVVGTTKIK +S EEGKNL+PNQQ	685
Sbjct	542	NLDQVTTESSYAMPSIKDISPGELAETLRRNIVQPIVVGTTKIKETSVEEGKNLSPNQQ	601
Query	686	VLIISDKAEEVPDMYWTKETAETLAKWLNIELEFQGSGSTVQKQDVRRANTAIKDICKIT VLIISDKAEEVPDMYWTKETAET AKWLNIELEF+GSGSTVQKQDVRRANTAIKDICKIT	745
Sbjct	602	VLIISDKAEEVPDMYWTKETAETFAKWLNIELEFEGSGSTVQKQDVRRANTAIKDICKIT	661
Query	746	LTLGD 750	
Sbjct	662	LTLGD 666	

>gb|AAN32860.1| penicillin-binding protein 2X [Streptococcus pneumoniae]
Length=661

Score = 1174 bits (3038), Expect = 0.0, Method: Composition-based stats.
Identities = 609/661 (92%), Positives = 635/661 (96%), Gaps = 0/661 (0%)

Query	90	DATSYNVYAVIDENYKSATGKILYVEKTQFNKVAEVFKYLDMEESYVREQLSQPNLKQV DATSYNVYAVIDENYKSATGKILYVEKTQFNKVAEVFKYLDMEESYVREQLSQPNLKQV	149
Sbjct	1	DATSYNVYAVIDENYKSATGKILYVEKTQFNKVAEVFKYLDMEESYVREQLSQPNLKQV	60
Query	150	SFGAKGNGITYANMMSIKKELEAAEVKGIDFTTSPNRNSYPNGQFASSFIGLAQLHENEDG SFG+KGNIGITYANMM+IKKELE AEVKGIDFTTSPNRNSYPNGQFASSFIGLAQLHENEDG	209
Sbjct	61	SFGSKGNGITYANMMAIKKELEAAEVKGIDFTTSPNRNSYPNGQFASSFIGLAQLHENEDG	120
Query	210	SKSLLGTSGMESSLNSILAGTDGIITYEKDRLGNIVPGTEQVSORTMDGKDVTYTTISSPL SKSLLGTSGMESSLNSILAG DGIITYEKDRLGNIVPGTEQVSQ+T+DGKDVTYTTISS L	269
Sbjct	121	SKSLLGTSGMESSLNSILAGKDGIIITYEKDRLGNIVPGTEQVSQQTVDGKDVTYTTISSTL	180
Query	270	QSFMETQMDAFQEKVKGKYMTATLVSAKTGEILATTQRPTFDADTKEGITEDFVWRDILY QSFMETQM+AFQEKVKGKYMTATLVSAKTGEILATTQRPTFDADTKEG+T+DFVWRDILY	329
Sbjct	181	QSFMETQMNAFQEKVKGKYMTATLVSAKTGEILATTQRPTFDADTKEGLTKDVFVWRDILY	240
Query	330	QSNYEPGSTMVKVMMIAAAIDNNTFPGEVFNSSELKIADATIRDWDVNNEGLTGGRMMTFS QSNYEPGSTMVKVMMIAAAIDNNTFPGEVFNSSELK+ADATIRDWDVNNEGLTGG MMTFS	389
Sbjct	241	QSNYEPGSTMVKVMTLAAAIDNNTFPGEVFNSSELKVADATIRDWDVNNEGLTGGMMTFS	300
Query	390	QGFAHSSNVGMTLLEQKMGDATWLDYLNRFKFGVPTRFGLTDEYAGQLPADNIVNIAQSS QGFAHSSNVGMTLLEQKMGDATWLDYLNRFKFG+PTRFGLTDEYAGQLPADNIVNIAQSS	449
Sbjct	301	QGFAHSSNVGMTLLEQKMGDATWLDYLNRFKFGIPTRFGLTDEYAGQLPADNIVNIAQSS	360
Query	450	FGQGISVTQTMIRAFATAIANDGVMLEPKFISAIYDPNDQTARKSQKEIVGNPVS KDAAS FGQGISVTQTMIRAFATAIANDGVMLEPKFI+A+YDPN+Q+ RKSQKEIVGNPVS KDAAS	509
Sbjct	361	FGQGISVTQTMIRAFATAIANDGVMLEPKFITALYDPNNQSVRSQKEIVGNPVS KDAAS	420
Query	510	LTRTNMVLVGTDPVYGTMYNHSTGKPTVTVPQNVALKSGTAQIADEKNGGYLVGLTDYI TRT+MVLVGTDP YGTMYNHSTGK TV VPGQNVALKSGTA+IADEKNGGYLVG T+ I	569
Sbjct	421	QTRTHMVLVGTDPRYGTMYNHSTGKATVNPGQNVALKSGTAEIADAEKNGGYLVGSTNNI	480
Query	570	FSAVSMSPAENPDFILYVTVQQPEHYSGIQLGEFANPILERASAMKDSLNLQTTAKALEQ FS V+M+PAENPDFILYVTVQQPEHYSGIQLGEFANPILERAMKDSLNLQ+TAK L+Q	629
Sbjct	481	FSVVMNPAENPDFILYVTVQQPEHYSGIQLGEFANPILERAVAMKDSLNLQSTAKLDQ	540
Query	630	VSQQSPYPMPSVKDISPGDLAEEELRRNLVQPIVVGTTKIKNSSAEKGKNLAPNQQVLIL V+ QS Y MPS+KDISPGDLAE LRRN+VQPIVVGTTKIK SS EEG NLAPNQQVL+L	689
Sbjct	541	VTNQSAVAMPSIKDISPGDLAEALRRNIVQPIVVGTTKIKESSVEEGSNLAPNQQVLL	600
Query	690	SDKAEEVPDMYWTKETAETLAKWLNIELEFQGSGSTVQKQDVRRANTAIKDICKITL LG SDKAEEVPDMYWTK TAE +KWLNIEL F+GSGSTVQKQDVRRANTAIKDICKITL LG	749
Sbjct	601	SDKAEEVPDMYWTKATAEAFSKWLNIELVFEFGSGSTVQKQDVRRANTAIKDICKITL LG	660
Query	750	D 750	

Sbjct 661 D 661

>gb|AYY56839.1| penicillin-binding protein 2X [Streptococcus pneumoniae]
Length=670

Score = 1170 bits (3027), Expect = 0.0, Method: Composition-based stats.
Identities = 603/670 (90%), Positives = 636/670 (94%), Gaps = 0/670 (0%)

Query 81	DRNGVPIAEDATSYNVYAVIDENYSATGKILYVEKTQFNKVAEVFHKYLDMEESYVREQ	140
Sbjct 1	DRNGVPIAEDATSYNVYAVIDENYSATGKILYVEKTQFNKVAEVFHKYLDMEESYVREQ	60
Query 141	LSQPNLKQVSFGAKGNIGITYANMMSIKKELEAAEVKGIDFTTSPNRSPNGQFASSFIGL	200
Sbjct 61	LSQPNLKQVSFGAKGNIGITYANMMSIKKELEAAEVKGIDFTTSPNRSPNGQFASSFIGL	120
Query 201	AQLHENEDGSKSLLGTSGMESSLNSILAGTDGIITYEKDRLGNIVPGTEQVSQRTMDGKD	260
Sbjct 121	AQLHENEDGSKSLLGTSGMESSLNSILAGTDGIITYEKDRLGNIVPGTEQVSQRTMDGKD	180
Query 261	VYTTISSLQSFMETQMDAFQEKVKGKYMATAVLVSAKTGEILATTQRPTFDADTKEGITE	320
Sbjct 181	VYTTISSLQSFMETQMDAF EKVKGKYMATAVLVSAKTGEILATTQRPTF+ADTKEGITE	240
Query 321	DFVWRDILYQSNEYEPGSTMKVMMLAAAIDNNTFPGGEVFNSSELKIADATIRDWDVNNEGL	380
Sbjct 241	DFVWRDILYQSNEYEPGS MKVM LA++IDNNTFP GE FNSSE KIADAT RDWDVN+GL	300
Query 381	TGGRMMTFSQGFAHSSNVGMTLLEQKMGDATWLDYLNRFKFGVPTRFGLTDEYAGQLPAD	440
Sbjct 301	TGGRMMTFLQGFAHSSNVGMSLLEQKMGDATWLDYLKRFKFGVPTRFGLTDEYAGQLPAD	360
Query 441	NIVNIAQSSFGQGISVTQTQMIRAFTAIANDGVMLEPKFISAIYDPNDQTARKSQKEIVG	500
Sbjct 361	NIVNIAQSSFGQGISVTQTQM+RAFTAIANDGVMLEPKFISAIYD N+Q+ RKSQKEIVG	420
Query 501	NPVSKDAASLTRNMVLVGTDPVYGTMYNHSTGKPTVTVPQNVALSGTAQIADEKNGG	560
Sbjct 421	NPVSK+AAS TR +M+LVGTD+YGTMYNH TGKP +TVPGQNV+A KSGTAQIADEKNGG	480
Query 561	YLVGLTDYIFSAVSMSPAENPDFILYVTVQQPEHYSGIQLGEFANPILERASAMKDSLNL	620
Sbjct 481	YLVG T+YIFS V+M+PAENPDFILYVTVQQPEHYSGIQLGEFA PILERASAMK+SLNL	540
Query 621	QTTAKALEQVSQQSPYPMPSVKDISPGDLAEELRRNLVQPIVVGTGTKIKKNSSAEEGKNL	680
Sbjct 541	Q+ AK L++V+ +S Y MPS+KDISPG+LAE LRRN+VQPIVVGTGTKIK +S EEG NL	600
Query 681	APNQQVLILSDKAEEVPDMYGWTKETAETLAKWLNLIEFQGSGSTVQKQDVRANTAIKD	740
Sbjct 601	APNQQVL+LSDK EE+PDMDYW KETAET AKWL+IELEF+GSWS VQKQDVR NTAIK+	660
Query 741	IKKITLTLGD 750	
Sbjct 661	IKKITLTLGD 670	

>emb|CAB65445.1| penicillin binding protein 2x [Streptococcus pneumoniae]
Length=666

Score = 1170 bits (3026), Expect = 0.0, Method: Composition-based stats.
Identities = 599/665 (90%), Positives = 636/665 (95%), Gaps = 0/665 (0%)

Query 85	VPIAEDATSYNVYAVIDENYSATGKILYVEKTQFNKVAEVFHKYLDMEESYVREQLSQP	144
Sbjct 1	VPIAEDATSYNVYAVIDENYSATGKILYVE+TQFNKVAEVFHKYLDMEESYVREQLSQP	60
Query 145	NLKQVSFGAKGNIGITYANMMSIKKELEAAEVKGIDFTTSPNRSPNGQFASSFIGLAQLH	204
Sbjct 61	NLKQVSFG+KGNGITYANMM++KKELE AEVKGIDFTTSPNRSPNGQFASSFIGLAQLH	120
Query 205	ENEDGSKSLLGTSGMESSLNSILAGTDGIITYEKDRLGNIVPGTEQVSQRTMDGKDVT	264
Sbjct 121	ENEDGSKSLLGTSGMESSLNSILAGTDGIITYEKDRLGNIVPGTEQVSQRTMDGKDVT	180
Query 265	ISSPLQSFMETQMDAFQEKVKGKYMATAVLVSAKTGEILATTQRPTFDADTKEGITEDFWW	324
Sbjct 181	+SSPLQSFMETQMDAF EKVKGKYMATAVLVSAKTGEILATTQRPTF+ADTK+GIT+DFWW	240
Query 325	RDILYQSNEYEPGSTMKVMMLAAAIDNNTFPGGEVFNSSELKIADATIRDWDVNNEGLTGGR	384
Sbjct 241	RDILYQSNEYEPGS MKVM LAA+IDNNTFPGE FNSSELKIADATIRDWDVN+GLT G	300
Query 385	MMTFSQGFAHSSNVGMTLLEQKMGDATWLDYLNRFKFGVPTRFGLTDEYAGQLPADNIVN	444

Sbjct	301	MMTFSQGFAHSSNVGM+LLEQKMGD TWLDYLNRFKFGVPTRFGLTDEY+GQLPADNIVN MMTFSQGFAHSSNVGMSLLEQKMGDTTWLDYLNRFKFGVPTRFGLTDEYSGQLPADNIVN	360
Query	445	IAQSSFGQGISVTQTOMIRAFTAIANDGVMLEPKFISAIYDPNDQTARKSQKEIVGNPVS IA S+FGQGISVTQTOM+RAFTAIA ANDGVMLEPKFISAIYD N+Q+ RKSQKEIVG PVS	504
Sbjct	361	IAMSAGFGQGISVTQTOMIRAFTAIANDGVMLEPKFISAIYDTNNQSVRKSQKEIVGKPVS	420
Query	505	KDAASLTTRTNMVLVGTDPVYGTMYNHSTGKPTVTVPGQNVALKSGTAQIADEKNGGYLVG +DAASLTTRTNM+LVGTD+YGTMYNH TGKP +TVPGQNVALKSGTA+IADEKNGGYLVG	564
Sbjct	421	EDAASLTTRTNMILVGTDPLYGTMYNHGTGPIITVPGQNVALKSGTAEIADEKNGGYLVG	480
Query	565	LTDYIFSAVSMSPAENPDFILYVTVQQPEHYSGIQLGEFANPILERASAMKDSLNLQTTA T+YIF V+M+PAENPDFILYVTVQQPEHYSGIQLGEFANPILERASAMK+SLNLQ+ A	624
Sbjct	481	STNYIIPVVTMNPENAEPDFILYVTVQQPEHYSGIQLGEFANPILERASAMKESLNLQSPA	540
Query	625	KALEQVSSQSPYPMPSVKDISPGDLAEELRRNLVQPIIVVGTGKIKNSSAEGKNLAPNQ K L+QV+ +S Y MPS+KDISPGDLAE LRRN+VQPIIVVGTGKIK SS EEG NLAPNQ	684
Sbjct	541	KNLDQVTTESSYAMPSIKDISPGDLAEALRRNIVQPIIVVGTGKIKESSVEEGTNLAPNQ	600
Query	685	QVLILSDKAAEVPDMDYWTKETAETLAKWLNLIEFQGSGSTVQKQDVRANTAIKDIKKI QV++LSDK EE+PDMDYGW KETAET AKWLNLIEF+GSGSTVQKQDVRANTAIKDIKKI	744
Sbjct	601	QVILLSDKVEEIIPDMYGWKETAETFAKWLNLIEFEGSGSTVQKQDVRANTAIKDIKKI	660
Query	745	TLLTG 749	
Sbjct	661	TLLTG 665	

>emb|CAA67013.1| penicillin-binding protein [Streptococcus pneumoniae]
Length=666

Score = 1169 bits (3024), Expect = 0.0, Method: Composition-based stats.
Identities = 602/666 (90%), Positives = 633/666 (95%), Gaps = 0/666 (0%)

Query	85	VPIAEDATSYNVYAVIDENYKSATGKILYVEKTQFNKVAEVFKYLDMEESYVREQLSQP VPIAEDATSYNVYAVIDENYKSATGKILYVEKTQFNKVAEVFKYL MEESYVREQLSQP	144
Sbjct	1	VPIAEDATSYNVYAVIDENYKSATGKILYVEKTQFNKVAEVFKYLAMEESYVREQLSQP	60
Query	145	NLKQVSFGAKGNGITYANMMSIKKELEAAEVKGIDFTTSPNRSYPNGQFASSFIGLAQLH NLKQVSFGAKGNGITYANMM+IKKELE AEVKGIDFTTSPNRSYPNGQFASSFIGLAQLH	204
Sbjct	61	NLKQVSFGAKGNGITYANMMAIKKELEAAEVKGIDFTTSPNRSYPNGQFASSFIGLAQLH	120
Query	205	ENEDGSKSLLGTSGMESSLNSILAGTDGIITYEKDRGNIVPGTEQVSORTMDGKDVTYTT ENEDGSKSLLGTSGMESSLNSILAGTDGIITYEKDR+GNIVPGTE VSQ+T+DGKDVTYTT	264
Sbjct	121	ENEDGSKSLLGTSGMESSLNSILAGTDGIITYEKDRVGNIVPGTELVSQQTVDGKDVTYTT	180
Query	265	ISSPLQSFMETQMDAFQEKVKGKYMATTLSAKTGEILATTQRTFDADTKEGITEDFVW +SSPLQSFMETQMDAF EKVKGKYMATTLSAKTGEILATTQRTFDADTK+GIT+DFVW	324
Sbjct	181	LSSPLQSFMETQMDAFLEKVKGKYMATTLSAKTGEILATTQRTFDADTKDGFITKDFVW	240
Query	325	RDILYQSNYEPGSTMVKVMMLAAAIDNNTFPGGEVFNSSELKIADATIRDWDVNNEGLTGGR RDILYQ NYEPGS MKVMMMA++IDNNTFPGGE FNSSE KIAD T RDWDVNNEGLTGGR	384
Sbjct	241	RDILYQGNYEPGSAMKVMMЛАСИДННTFPGGEYFNSESКIADVTTRDWDVNNEGLTGГГ	300
Query	385	MMTFSQGFAHSSNVGMLLLEQKMGDATWLDYLNRFKFGVPTRFGLTDEYAGQLPADNIVN MMTFSQGFAHSSNVGM LLE+KMGD TWLDYLNRFKFGVPTRFGLTDEYAGQLPADNIV+	444
Sbjct	301	MMTFSQGFAHSSNVGMLLLEEKMGDTTWLDYLNRFKFGVPTRFGLTDEYAGQLPADNIVS	360
Query	445	IAQSSFGQGISVTQTOMIRAFTAIANDGVMLEPKFISAIYDPNDQTARKSQKEIVGNPVS IAQSSFGQGISVTQTOMIRAFTAIANDGVMLEPKFI+A+YDPNDQT RKSQKEIVGNPVS	504
Sbjct	361	IAQSSFGQGISVTQTOMIRAFTAIANDGVMLEPKFITALYDPNDQTVRKSQKEIVGNPVS	420
Query	505	KDAASLTTRTNMVLVGTDPVYGTMYNHSTGKPTVTVPGQNVALKSGTAQIADEKNGGYLVG KDAAS TRT MVLVGTDPVYGTMYNHSTGKPTVTVPGQNVALKSGTAQIADEKNGGYLVG	564
Sbjct	421	KDAASQRTQMVLTGTDVYGTMYNHSTGKPTVTVPGQNVALKSGTAQIADEKNGGYLVG	480
Query	565	LTDYIFSAVSMSPAENPDFILYVTVQQPEHYSGIQLGEFANPILERASAMKDSLNLQTTA T+YIFS V+M+PAENPDFILYVTVQQPEHYSGIQLGEFANPILERASAMK+SLNLQ+ A	624
Sbjct	481	PTNYIHSVAMNPENAEPDFILYVTVQQPEHYSGIQLGEFANPILERASAMKESLNLQSPA	540
Query	625	KALEQVSSQSPYPMPSVKDISPGDLAEELRRNLVQPIIVVGTGKIKNSSAEGKNLAPNQ K L+QV+ +S Y MPS+KDISPG+LAE LRRN+VQPIIVVGTGKIK +S EEGKNLAPNQ	684
Sbjct	541	KNLDQVTTESSYAMPSIKDISPGELAETLRRNIVQPIIVVGTGKIKETSVEEGKNLAPNQ	600
Query	685	QVLILSDKAAEVPDMDYWTKETAETLAKWLNLIEFQGSGSTVQKQDVRANTAIKDIKKI QVL+LSDK EE+PDMDYGW KETAET AKWL+IEF+GSGS VQKQDVR NTAIK+IKKI	744
Sbjct	601	QVLLSDKVEEIIPDMYGWKETAETFAKWL DIEFEGSGSIVQKQDVRTNTAIKNIKKI	660
Query	745	TLLGD 750	
Sbjct	661	KLTLD 666	

>gb|AYA56838.1| penicillin-binding protein 2X [Streptococcus pneumoniae]
Length=670

Score = 1165 bits (3014), Expect = 0.0, Method: Composition-based stats.
 Identities = 601/670 (89%), Positives = 635/670 (94%), Gaps = 0/670 (0%)

Query	81	DRNGVPIAEDATSYNVAVIDENYKSATGKILYVEKTQFNKVAEVFKYLDMEESYVREQ	140
Sbjct	1	DRNGVPIAEDATSYNVAVIDENYKSATGKILYVEKTQFNKVAEVFKYLDMEESYVREQ	60
Query	141	LSQPNLKQVSFGAKGNIGITYANMMSIKKELEAAEVKGIDFTTSPNRSPNGQFASSFIGL	200
Sbjct	61	LSQPNLKQVSFGAKGNIGITYANMMSIKKELE AAEVKGIDFTTSPNRSPNGQFASSFIGL	120
Query	201	AQLHENEDGSKSLLGTSGMESSLNSILAGTDGIITYEKDRLGNIVPGTEQVSQRTMDGKD	260
Sbjct	121	AQLHENEDGSKSLLGTSGMESSLNSILAGTDGIITYEKDRLGNIVPGTEQVSQRTMDGKD	180
Query	261	VYTTISSLQSFMETQMDAFQEKVKGKYMATAVLVSAKTGEILATTQRPTF+ADTKEGITE	320
Sbjct	181	VYTTISSLQSFMETQMDAFQEKVKGKYMATAVLVSAKTGEILATTQRPTFNADTKEGITE	240
Query	321	DFVWRDILYQSNYEPGSTMVKVMMIAAIIDNNTFPGEVFNSSELKIADATIRDWDVNNEGL	380
Sbjct	241	DFVWRDILYQSNYEPGS MKVM LA++IDNNTFP GE FNSSE KIADAT RDWDVN+GL	300
Query	381	TGGRMMTFSQGFAHSSNVGMTLLEQKMGDATWLDYLNRFKFGVPTRFGLTDEYAGQLPAD	440
Sbjct	301	TGGRMMTFSQGFAHSSNVGM+LLEQKMGDATWLDYL RFKFGVPTRFGLTDEYAGQLPAD	360
Query	441	NIVNIAQSSFGQGISVTQTQMIRAFTAIANDGVMLEPKFISAIYDPNDQTARKSQKEIVG	500
Sbjct	361	NIVNIAQSSFGQGISVTQTQMIRAFTAIANDGVMLEPKFISAIYDTNNQSVRKSQKEIVG	420
Query	501	NPVSKDAASLTTRTNMVLVGTDPVYGTMYNHSTGKPTVTPGQNVALKSGTAQIADEKNGG	560
Sbjct	421	NPVSK+AAS TR +M+LVGTD+YGTMYNH TGKP +TPGQNVA+KSGTAQIADEKNGG	480
Query	561	YLVGLTDYIFSAVSMSPAENPDFILYVTVQQPEHYSGIQLGEFANPILERASAMKDSLNL	620
Sbjct	481	YLVGSTNYIFSVVTMNPENAENPDFILYVTVQQPEHYSGIQLGEFATPILERASAMKESLNL	540
Query	621	QTTAKALEQVSQQSPYPMPSVKDISPGDLAEELRRNLVQPIVVGTTGKIKNSSAEEGKNL	680
Sbjct	541	Q+ AK L++V+ +S Y MPS+KDISPG+LAE LRRN+VQPIVVGTTGKIK +S EEG NL	600
Query	681	APNQQVLILSDKAEEVPDMYGWTKETAETLAKWLNLIEFQGSGSTVQKQDVRANTAIKD	740
Sbjct	601	APNQQVL+LSDK EE+PDMDYGW KETAET AKWL+IELEF+GSGS VQKQDVRANTAIKD	660
Query	741	IKKITLTLGD 750	
Sbjct	661	IKKITLTLGD 670	

>emb|CAB65442.1| penicillin binding protein 2x [Streptococcus pneumoniae]
 Length=666

Score = 1165 bits (3014), Expect = 0.0, Method: Composition-based stats.
 Identities = 597/666 (89%), Positives = 630/666 (94%), Gaps = 0/666 (0%)

Query	85	VPIAEDATSYNVAVIDENYKSATGKILYVEKTQFNKVAEVFKYLDMEESYVREQLSQP	144
Sbjct	1	VPIAEDATSYNVAVIDENYKSATGKILYVEKTQFNKVAEVFKYLDMEESYVREQLSQP	60
Query	145	NLKQVSFGAKGNIGITYANMMSIKKELEAAEVKGIDFTTSPNRSPNGQFASSFIGLAQLH	204
Sbjct	61	NLKQVSFG+KGNGITYANMMSIKKELE AEVKGIDFTTSPNRSPNGQFASSFIGLAQLH	120
Query	205	ENEDGSKSLLGTSGMESSLNSILAGTDGIITYEKDRLGNIVPGTEQVSQRTMDGKDVT	264
Sbjct	121	ENEDGSKSLLGTSGMESSLNSILAGTDGIITYEKDRLGNIVPGTEQVSQRTMDGKDVT	180
Query	265	ISSPLQSFMETQMDAFQEKVKGKYMATAVLVSAKTGEILATTQRPTFDADTKEGITEDFVW	324
Sbjct	181	ISSLQSFMETQMDAFQEKVKGKYMATAVLVSAKTGEILATTQRPTFDADTKEGIT+DFVW	240
Query	325	RDILYQSNYEPGSTMVKVMMIAAIIDNNTFPGEVFNSSELKIADATIRDWDVNNEGLTGGR	384
Sbjct	241	RDILYQSNYEPGSTMVKVMMIAAIIDNNTFPGEVFNSSELKIADATIRDWDVNNEGLTGGR	300
Query	385	MMTFSQGFAHSSNVGMTLLEQKMGDATWLDYLNRFKFGVPTRFGLTDEYAGQLPADNIVN	444
Sbjct	301	MMTF QGFA SSNVGM+LLEQKMGDATWLDYLNRFKFGVPTRFGLTDEYAGQLPADNIVN	360
Query	445	IAQSSFGQGISVTQTQMIRAFTAIANDGVMLEPKFISAIYDPNDQTARKSQKEIVGNPVS	504
Sbjct	361	IAQSSFGQGISVTQTQMLRAFTAIANDGVMLEPKFITALYDPNDQTVRRSQKEIVGNPVS	420

Query	505	KDAASLRTNMLVGTDPVYGTMYNHSTGKPTVTVPQONVALKSGTAQIADEKNGGYLVG	564
Sbjct	421	KDAASLRTNMLVGTDPVYGTMYNHSTGKPTVTVPQONVALKSGTAQIADEKNGGYLVG	480
Query	565	LTDYIFSAVSMSPAENPDFILYVTVQQPEHYSGIQLGEFANPILERASAMKDSLNLQTTA T+YIFS VSM+PAENPDFILYVTVQQPEHYSGIQLGEFANPILERASAMK+SLNLQ+ A	624
Sbjct	481	ATNYIFSVVSMNPAENPDFILYVTIQQPEHYSVVHGEFANPILERASAMKESLNQSPA	540
Query	625	KALEQVSQQSPYPMPSPVKDISPGDLAEELRRNLVQPIVVGTGTKIKNSSAEEGKNLAPNQ K LEQV+ +S Y MPS+KDISPGDLAE LRRN+VQPIV+GTGTKIK SS EEGKNL PNQ	684
Sbjct	541	KNLEQVTAESSYAMPSIKDISPGDLAEALRRNIVQPIVIGTGTKIKESSVEEGKNLVPNQ	600
Query	685	QVLILSDKAAEVPDMYGTWTKETAETLAKWLNLIELEFQGSGSTVQKQDVRANTAIKDIKKI QVL+LSDK EE+PDMYGW KETAEE AKWL+IELEF+GSGS VQ+QDVRANT IK+IK I	744
Sbjct	601	QVLLLSDKVVEIPDMYGWKKETAEEFAKWL DIELEFEGSGSIVQQQDVRANTTIKNIKNI	660
Query	745	TTLGD 750	
Sbjct	661	KTLGD 666	

>emb|CAB65443.1| penicillin binding protein 2x [Streptococcus pneumoniae]
Length=666

Score = 1162 bits (3007), Expect = 0.0, Method: Composition-based stats.
Identities = 601/666 (90%), Positives = 634/666 (95%), Gaps = 0/666 (0%)

Query	85	VPIAEDATSYNVAVIDENYKSATGKILYVEKTQFNKVAEVFKYLDMEESYVREQLSQP	144
Sbjct	1	VPIAEDATSYNVAVIDENYKSATGKILYVEKTQFNKVAEVFKYLDMEESYVREQLSQP	60
Query	145	NLKQVSFGAKGNNGITYANMMSIKKELEAAEVKGIDFTTSPNRSPNGQFASSFIGLAQLH NLKQVSFGAKGNNGITYANMMSIKKELE AEVKGIDFTTSPNRSPNGQFASSFIGLAQLH	204
Sbjct	61	NLKQVSFGAKGNNGITYANMMSIKKELEAAEVKGIDFTTSPNRSPNGQFASSFIGLAQLH	120
Query	205	ENEDGSKSLLGTSQMMESSLNSILAGTDGIITYEKDRGNIVPGTEQVSORTMDGKDVT ENEDGSKSLLGTSQMMESSLNSILAG DGIITYEKDRGNIVPGTEQVSQ+T+DGKDVT	264
Sbjct	121	ENEDGSKSLLGTSQMMESSLNSILAGKDGIIITYEKDRGNIVPGTEQVSQQTVDGKDVT	180
Query	265	ISSPLQSFMETQMDAFQEKVKGKYMATTLSAKTGEILATTQRPTFDADTKEGITEDFW ISS LQSFMETQMDAFQEKVKGKYMATTLSAKTGEILATTQRPTFDADTKEG+T+DFW	324
Sbjct	181	ISSTLQSFMETQMDAFQEKVKGKYMATTLSAKTGEILATTQRPTFDADTKEGLTDFW	240
Query	325	RDILYQSNEYEPGSTMKVMMLAAAIDNNTFPGGEVFNSSELKIADATIRDWDVNNEGLTGGR RDILYQSNEYEPGSTMKVM LA++ID+NTFP GE FNNSSELKIADATIRDWDVN+GLT G	384
Sbjct	241	RDILYQSNEYEPGSTMKVMTLASSIDSNTFPSGEYFNNSSELKIADATIRDWDVNNDGLTTGG	300
Query	385	MMTFSQGFAHSSNVGMTLLEOKMGDATWLDYLNRFKFGVPTRFGLTDEYAGQLPADNIVN MMTF QGFA+SSNVGM+LLEOKMGDATWLDYLNRFKFGVPTRFGLTDEY+GQLPADNIVN	444
Sbjct	301	MMTFLQGFAYSSNVGMSLLEOKMGDATWLDYLNRFKFGVPTRFGLTDEYSGQLPADNIVN	360
Query	445	IAQSSFGQGISVTQTQMIRAFTAIANDGVMLEPKFISAIYDPNDQTARKSQKEIVGNPVS IA S+FGQGISVTQTQMIRAFTAIANDGVMLEPKFISA+YDPNDQT RKSQKEIVGNPVS	504
Sbjct	361	IAMSAGFGQGISVTQTQMLRAFTAIANDGVMLEPKFISALYDPNDQTVRKSQKEIVGNPVS	420
Query	505	KDAASLRTNMLVGTDPVYGTMYNHSTGKPTVTVPQONVALKSGTAQIADEKNGGYLVG KDAAS TRT+MVLVGTDP YGTMYNHSTGK TV VPQONVALKSGTA+IADEKNGGYLVG	564
Sbjct	421	KDAASQTRTHMLVGTDPYGTMYNHSTGKATVNPQONVALKSGTAEIADEKNGGYLVG	480
Query	565	LTDYIFSAVSMSPAENPDFILYVTVQQPEHYSGIQLGEFANPILERASAMKDSLNLQTTA T+YIFS V+M+PAENPDFILYVTVQQPEHYSGIQLGEFANPILERASAMK+SLNLQ+ A	624
Sbjct	481	STNYIFSVVAMNPAENPDFILYVTVQQPEHYSGIQLGEFANPILERASAMKESLNQSPA	540
Query	625	KALEQVSQQSPYPMPSPVKDISPGDLAEELRRNLVQPIVVGTGTKIKNSSAEEGKNLAPNQ K L+QV+ +S Y MPS+KDISPG+LAE LRRN+VQPIVVGTGTKIK +S EEGKNLAPNQ	684
Sbjct	541	KNLDQVTTESSYAMPSIKDISPGELAEALRRNIVQPIVVGTGTKIKETSVEEGKNLAPNQ	600
Query	685	QVLILSDKAAEVPDMYGTWTKETAETLAKWLNLIELEFQGSGSTVQKQDVRANTAIKDIKKI QVL+LSDK EE+PDMYGW KETAEE AKWL+IELEF+GSGS VQKQDVR NTAIK+IKKI	744
Sbjct	601	QVLLLSDKVVEIPDMYGWKKETAEEFAKWL DIELEFEGSGSIVQKQDVRTNTAIKNIKCI	660
Query	745	TTLGD 750	
Sbjct	661	KTLGD 666	

>gb|AYA56842.1| penicillin-binding protein 2X [Streptococcus pneumoniae]
Length=669

Score = 1160 bits (3000), Expect = 0.0, Method: Composition-based stats.
Identities = 597/669 (89%), Positives = 633/669 (94%), Gaps = 0/669 (0%)

Query	82	RNGVPIAEDATSYNVAVIDENYKSATGKILYVEKTQFNKVAEVFKYLDMEESYVREQL	141
Sbjct	1	RNGVPIAEDATSYNVAVIDENYKSATGKILYVEKTQFNKVAEVFKYLDMEESYVREQL	60

Query	142	SQPNLKQVSFGAKGNIGITYANMMSIKKELEAAEVKGIDFTTSPNRSYPNGQFASSFIGLA	201
Sbjct	61	SQPNLKQVSFGAKGNIGITYANMM+IKKELE AEVKGIDFTTSPNRSYPNGQFASSFIGLA	120
Query	202	QLHENEDGSKSLLGTSGMESSLNSILAGTDGIITYEKDRLGNIVPGTEQVSQRTMDGKDV	261
Sbjct	121	QLHENEDGSKSLLGTSGMESSLNSILAGTDGIITYEKDRLGNIVPGTEQVSQQTVDGKDV	180
Query	262	YTTISSLQSFMETQMDAFQEKVKGKYMATLVSAKTGEILATTQRPTFDADTKEGITED	321
Sbjct	181	YTTISSLQSFMETQMDAF EKVKGKYMATLVSAKTGEILATTQRPTF+ADTKEGITED	240
Query	322	FVWRDILYQSNYEPGSTMVKVMMIAAAIDNNTFPGGEVFNSSELKIADATIRDWDVNNEGLT	381
Sbjct	241	FVWRDILYQSNYEPGS MKVM LA++IDNNTFP GE FNSSE KIADAT RDWDVN+GLT	300
Query	382	GGRMMTFSQGFAHSSNVGMTLLEQKMGDATWLDYLNRFKFGVPTRFGLTDEYAGQLPADN	441
Sbjct	301	TGGMMTFLQGFAHSSNVGMSLLEQKMGDATWLDYLKRKFKGVPTRFGLTDEYAGQLPADN	360
Query	442	IVNIAQSSFGQGISVTQTQMIRAFTAIANDGVMLEPKFISAIYDPNDQTARKSQKEIVGN	501
Sbjct	361	IVSIAQSSFGQGISVTQTQM+RAFTAIA ANDGVMLEPKFISAIYD N+Q+ RKSQKEIVGN	420
Query	502	PVSKDAASLTRTNMVLVGTDPPVYGTMYNHSTGKPTVTVPQNVALKSGTAQIADEKNGGY	561
Sbjct	421	PVSK+AAS TR +M+LVGTDPP+YGTMYNH TGKP +TVPGQNVVA+KSGTAQIADEKNGGY	480
Query	562	LVLGTDYIFSAVSMSPAENPDFILYVTVQQPEHYSGIQLGEFANPILERASAMKDSLNLQ	621
Sbjct	481	LVLG T+YIFS V+M+PAENPDFILYVTVQQPEHYSGIQLGEFA PILERASAMK+SLNLQ	540
Query	622	TTAKALEQVSQQSPYPMPSVKDISPGDLAELRRNLVQPIVVGTGKIKKNSSAEEGKNLA	681
Sbjct	541	+ AK L++V+ +S Y MPS+KDISPG+LAE LRRN+VQPIVVGTGKIK +S EEG NLA SPAKNLDKVTESSYAMPSIKDISPGELAEALRRNIVQPIVVGTGKIKETSVEEGTNLA	600
Query	682	PNQQVLILSDKAEEVPDMYGWTKETAETLAKWLNIIELEFQGSGSTVQKQDVRANTAIKDI	741
Sbjct	601	PNQQVL+LSDK EE+PDMYGW KETAET AKWL+IELEF+GSGS VQKQDVR NTAIK+I	660
Query	742	KKITLTLGD 750	
Sbjct	661	KKIKLTLGD 669	

>gb|AY56852.1| penicillin-binding protein 2X [Streptococcus pneumoniae]
Length=670

Score = 1158 bits (2996), Expect = 0.0, Method: Composition-based stats.
Identities = 596/670 (88%), Positives = 632/670 (94%), Gaps = 0/670 (0%)

Query	81	DRNGVPIAEDATSYNVYAVIDENYKSATGKILYVEKTQFNKVAEVFKYLDMEESYVREQ	140
Sbjct	1	DRNGVPIAEDATSYNVYAVIDENYKSATGKILYVEKTQFNKVAEVFKYLDMEESYVREQ	60
Query	141	LSOPNLKQVSFGAKGNIGITYANMMSIKKELEAAEVKGIDFTTSPNRSYPNGQFASSFIGL	200
Sbjct	61	LSOPNLKQVSFGAKGNIGITYANMM+IKKELE AEVKGIDFTTSPNRSYPNGQFASSFIGL	120
Query	201	AQLHENEDGSKSLLGTSGMESSLNSILAGTDGIITYEKDRLGNIVPGTEQVSQRTMDGKD	260
Sbjct	121	AQLHENEDGSKSLLGTSGMESSLNSILAGTDGIITYEKDRLGNIVPGTEVSQ+T+DGKD	180
Query	261	VYTTISSLQSFMETQMDAFQEKVKGKYMATLVSAKTGEILATTQRPTFDADTKEGITE	320
Sbjct	181	VYTT+SSPLQSFMETQMDAF EKVKGKYMATLVSAKTGEILATTQRPTF+ADTKEGITE	240
Query	321	DFVWRDILYQSNYEPGSTMVKVMMIAAAIDNNTFPGGEVFNSSELKIADATIRDWDVNNEGL	380
Sbjct	241	DFVWRDILYQSNYEPGS KVMMIA++IDNNTFP GE FNSSE KIADAT RDWDVNNEGL	300
Query	381	TGGRMMTFSQGFAHSSNVGMTLLEQKMGDATWLDYLNRFKFGVPTRFGLTDEYAGQLPAD	440
Sbjct	301	TGGMMTFSQGFAHSSNVGTSLLLEQKMGDATWLDYLKRKFKGVPTRFGLTDEYAGQLPAD	360
Query	441	NIVNIAQSSFGQGISVTQTQMIRAFTAIANDGVMLEPKFISAIYDPNDQTARKSQKEIVG	500
Sbjct	361	NIVSIAQSSFGQGISVTQTQM+RAFTAIA ANDGVMLEPKFISAIYD N+Q+ RKSQKEIVG	420
Query	501	NPVSKDAASLTRTNMVLVGTDPPVYGTMYNHSTGKPTVTVPQNVALKSGTAQIADEKNGG	560
Sbjct	421	NPVSK+AAS TR +M+LVGTDPP+YGTMYNH TGKP +TVPGQNVVA+KSG AQIADEKNGG	480
Query	561	YLVGLTDYIFSAVSMSPAENPDFILYVTVQQPEHYSGIQLGEFANPILERASAMKDSLNL	620
Sbjct	481	YLVGSTNYIFSVVTMNPAAENPDFILYVTVQQPEHYSGIQLGEFATPILERASAMKESLN	540

Query	621	QTTAKALEQVSQQSPYPMPSVKDISPGDLAEEELRRNLVQPIVVGTGKIKNSSAEEGKNL Q+ AK L++V+ +S Y MPS+KDISPG+LAE LRRN+VQPIVVGTGKIK +S EEG NL	680
Sbjct	541	QSPAQNLDKVTESSYAMPSIKDISPGELAEALRRNIVQPIVVGTGKIKETSVEEGTNL	600
Query	681	APNQQVLILSDKAEEVPDMYGWTKETAETLAKWLNLIEFQGSGSTVQKQDVRANTAIKD APNQQVL+LSDK EE+PDMYGW KETAET AKWL+IELEF+GSGS VQKQDVR NTAIK+	740
Sbjct	601	APNQQVLLLSDKVEEI PDMYGWKKETAETFAKWLDIELEFEGSGSVVQKQDVRNTAIKN	660
Query	741	IKKITLTLD 750	
Sbjct	661	IKKIKLTLD 670	

>emb|CAB65441.1| penicillin binding protein 2x [Streptococcus pneumoniae]
Length=666

Score = 1157 bits (2992), Expect = 0.0, Method: Composition-based stats.
Identities = 597/666 (89%), Positives = 631/666 (94%), Gaps = 0/666 (0%)

Query	85	VPIAEDATSYNVYAVIDENYKSATGKILYVEKTQFNKVAEVFKYLDMEESYVREQLSQP VPIAEDATSYNVYAVIDENYKSATGKILYVEKTQFNKVAEVFKYLDMEESYVREQLSQP	144
Sbjct	1	VPIAEDATSYNVYAVIDENYKSATGKILYVEKTQFNKVAEVFKYLDMEESYVREQLSQP	60
Query	145	NLKQVSFGAKGNIGITYANMMSIKKELEAAEVKGIDFTTSPNRSPNGQFASSFIGLAQLH NLKQVSFGAKGNIGITYANMMSIKKELE AEVKGIDFTTSPNRSPNGQFASSFIGLAQLH	204
Sbjct	61	NLKQVSFGAKGNIGITYANMMSIKKELEAAEVKGIDFTTSPNRSPNGQFASSFIGLAQLH	120
Query	205	ENEDGSKSLGTSGMESSLNSILAGTDGIITYEKDRGLGNIVPGTEQVSQRTMDGKDVTYTT ENEDGSKSLGTSGMESSLNSILAG DGIITYEKDRGLGNIVPGTEQVSQ+T+DGKDVTYTT	264
Sbjct	121	ENEDGSKSLGTSGMESSLNSILAGKDGIIITYEKDRGLGNIVPGTEQVSQQTVDGKDVTYTT	180
Query	265	ISSPLQSFMETQMDAFQEVKVGKYMATTLSAKTGEILATTQRPTFDADTKEGITEDFVW ISS LQSFMETQMDAFQEVKVGKYMATTLSAKTGEILATTQRPTF+ADTKEGITEDFVW	324
Sbjct	181	ISSTLQSFMETQMDAFQEVKVGKYMATTLSAKTGEILATTQRPTFNADTKEGITEDFVW	240
Query	325	RDILYQSNYEPGSTMVMMLAAAIDNNTPGGEVFNSELKIADATIRDWDVNNEGLTGGR RDILYQSNYEPGS MKVM LA+IDNNTP GE FNSSE KIADAT RDWDVN+GLT G	384
Sbjct	241	RDILYQSNYEPGSAMKVMLASSIDNNTPPSGEYFNSSEFKIADATTRDWDVNNDGLTTGG	300
Query	385	MMTFSQGFAHSSNVGMILLEQKMGDATWLDPYLNRFKFGVPTRFGLTDEYAGQLPADNIVN MMTF QGFAHSSNVGM+LLEQKMGDATWLDPYLNRFKFGVPTRFGLTDEYAGQLPADNIV+	444
Sbjct	301	MMTFLQGFAHSSNVGMSLLEQKMGDATWLDPYLNRFKFGVPTRFGLTDEYAGQLPADNIVS	360
Query	445	IAQSSFGQGISVTQTQMIRAFTAIANDGVMLEPKFISAIYDPNDQTARKSQKEIVGNPVS IAQSSFGQGISVTQTQMIRAFTAIANDGVMLEPKFISAIYD N+Q+ RKSQKEIVGNPVS	504
Sbjct	361	IAQSSFGQGISVTQTQMLRAFTAIANDGVMLEPKFISAIYDTNNQSVRKSQKEIVGNPVS	420
Query	505	KDAASLRTNMVLVGTDPVYGTMYNHSTGKPTTVPGQONVALKSGTAQIADEKNGGYLVG K+AAS TR +M+LVGTD+YGTMYNH TGKP +TVPGQNV+KSGTAQIADEKNGGYLVG	564
Sbjct	421	KEAASSTTRNHHMILVGTDPYGTMYNHGTGKPIITVPGQNVAVKSGTAQIADEKNGGYLVG	480
Query	565	LTDYIFSAVSMSPAENPDFILYVTVQQPEHYSGIQLGEFANPILERASAMKDSLNLQTTA T+YIFS V+M+PAENPDFILYVTVQQPEHYSGIQLGEFA PILERASAMK+SLNLQ+ A	624
Sbjct	481	STNYIIFSVVTMNPAPAENPDFILYVTVQQPEHYSGIQLGEFATPILERASAMKESLNLQSPA	540
Query	625	KALEQVSSQSPYPMPSVKDISPGDLAEEELRRNLVQPIIVVGTGKIKNSSAEEGKNLAPNQ K L++V+ +S Y MPS+KDISPG+LAE LRRN+VQPIIVVGTGKIK +S EEG NLAPNQ	684
Sbjct	541	KNLDKVTESSYAMPSIKDISPGELAEALRRNIVQPIIVVGTGKIKETSVEEGTNLAPNQ	600
Query	685	OVLILSDKAAEVPDMYGWTKETAETLAKWLNLIEFQGSGSTVQKQDVRANTAIKDIKKI OVL+LSDK EE+PDMYGW KETAET AKWL+IELEF+GSGS VQKQDVRANTAIKDIKKI	744
Sbjct	601	OVLILSDKAAEVPDMYGWTKETAETLAKWLNLIEFQGSGSTVQKQDVRANTAIKDIKKI OVL+LSDK EE+PDMYGW KETAET AKWL+IELEF+GSGS VQKQDVRANTAIKDIKKI	660
Query	745	TTLGD 750	
Sbjct	661	TTLGD 666	

>gb|AAN32855.1| penicillin-binding protein 2X [Streptococcus pneumoniae]
Length=661

Score = 1157 bits (2992), Expect = 0.0, Method: Composition-based stats.
Identities = 598/661 (90%), Positives = 630/661 (95%), Gaps = 0/661 (0%)

Query	90	DATSYNVYAVIDENYKSATGKILYVEKTQFNKVAEVFKYLDMEESYVREQLSQPNLKQV DATSYNVYAVIDENYKSATGKILYVEKTQFNKVAEVFKYLDMEESYVREQLSQPNLKQV	149
Sbjct	1	DATSYNVYAVIDENYKSATGKILYVEKTQFNKVAEVFKYLDMEESYVREQLSQPNLKQV	60
Query	150	SFGAKGNIGITYANMMSIKKELEAAEVKGIDFTTSPNRSPNGQFASSFIGLAQLHENEDG SFGAKGNIGITYANMMSIKKELE AEVKGIDFTTSPNRSPNGQFASSFIGLAQLHENEDG	209
Sbjct	61	SFGAKGNIGITYANMMSIKKELEAAEVKGIDFTTSPNRSPNGQFASSFIGLAQLHENEDG	120
Query	210	SKSLLGTSGMESSLNSILAGTDGIITYEKDRGLGNIVPGTEQVSQRTMDGKDVTYTTISPL SKSLLGTSGMESSLNSILAGTDGIITYEKDRGLGNIVPGTEQVSQ+T+DGKDVTYTTISL	269
Sbjct	121	SKSLLGTSGMESSLNSILAGTDGIITYEKDRGLGNIVPGTEQVSQQTVDGKDVTYTTISL	180

Query	270	QSFMETQMDAFQEKVKGKYMTATLVSAGTGEILATTORPTFDADTKEGITEDFVWRDILY	329
Sbjct	181	QSFMETQMDAFQEKVKGKYMTATLVSAGTGEILATTQRPTFDADTKEG+T+DFVWRDILY	240
Query	330	QSNYEPGSTMVKVMMMLAAAIDNNTFPGEVFNSSELKIAADATIRDWDVNNEGLTGGRMMTFS	389
Sbjct	241	QSNYEPGSTMVKVLA++IDNNTFPGEFNSSELKIAADATIRDWDVN+GLT G MMTF	300
Query	390	QGFAHSSNVGMTLLEQKMGDATWLDYLNRFKFGVPTRFGLTDEYAGQLPADNIVNIAQSS	449
Sbjct	301	QGFA+SSNVGM+LLEQKMGDATWLDYLNRFKFGVPTRFGLTDEY+GQLPADNIVNIA S+	360
Query	450	FGQQGISVTQTQMIRAFTAIANDGVMLEPKFISAIYDPNDQTARKSQKEIVGNPVSCKDAAS	509
Sbjct	361	FGQQGISVTQTQM+RAFTAIANDGVMLEPKFISA+YDPNDQT RKSQKEIVGNPVSCKDAAS	420
Query	510	LTRTNMVLVGTDPVYGTMYNHSTGKPTVTVPQONVALKSGTAQIADEKNGGYLVGLTDYI	569
Sbjct	421	TRT+MVLVGTDP YGTMYNHSTGK TV VPGQONVALKSGTA+IADEKNGGYLVG T+YI	480
Query	570	FSAVSMSPAENPDFILYVTVQQPEHYSGIQLGEFANPILERASAMKDSLNLQTTAKALEQ	629
Sbjct	481	FS V+M+PAENPDFILYVTVQQPEHYSGIQLGEFANPILERASAMK+SLNLQ+ AK L+Q	540
Query	630	VQQQSPYPMPSVKDISPGDLAEELRRLVQPIVVGTGKIKKNSSAEEGKNLAPNQQVLIL	689
Sbjct	541	V+ +S Y MPS+KDISPG+LAE LRRN+VQPIVVGTGKIK +S EEGKNLAPNQQVL+L	600
Query	690	SDKAEEVPDMYGTWTKETAETLAKWLNLIELEFQGSGSTVQKQDVRAKTAIKDIKKITLTG	749
Sbjct	601	SDK EE+PDGYGW KETAE AKWL+IELEF+GSGS VQKQDV NTAIK+IKKI LTG	660
Query	750	D 750	
Sbjct	661	D 661	

>gb|AYA56849.1| penicillin-binding protein 2X [Streptococcus pneumoniae]
Length=669

Score = 1155 bits (2987), Expect = 0.0, Method: Composition-based stats.
Identities = 594/669 (88%), Positives = 632/669 (94%), Gaps = 0/669 (0%)

Query	82	RNGVPIAEDATSINYAVIDENYSATGKILYVEKTQFNKVAEVFKYLDMEESYVREQL	141
Sbjct	1	RNGVPIAEDATSINYAVIDENYSATGKILYVEKTQFNKVAEVFKYLDMEESYVREQL	60
Query	142	SQPNLKQVSFGAKGNIGITYANMMSIKKELEAAEVKGIDFTTSPNRSYPNGQFASSFIGLA	201
Sbjct	61	SQPNLKQVSFG+KGNGITYANMMSIKKELE AEVKGIDFTTSPNRSYPNGQFASSFIGLA	120
Query	202	QLHENEDGSKSLLGTSGMESSLNSILAGTDGIITYEKDRLGNI VPGTEQVSQRTMDGKD	261
Sbjct	121	QLHENEDGSKSLLGTSGMESSLNSILAGTDGIITYEKDR+GNIVPGTE VSQ+T+DGKD	180
Query	262	YTTISSPLQSFMETQMDAFQEKVKGKYMTATLVSAGTGEILATTQRPTFDADTKEGITED	321
Sbjct	181	YTT+SSPLQSFMETQMDAF EKVKGKYMTATLVSAGTGEILATTQRPTF+ADTKEGITED	240
Query	322	FVWRDILYOSNYEPGSTMVKVMMMLAAAIDNNTFPGEVFNSSELKIAADATIRDWDVNNEG	381
Sbjct	241	FVWRDILYQSNYEPGS MKVM LA++IDNNTFP GE FNSSE KIADAT RDWDVN+GLT	300
Query	382	GGRMMTFSQGFAHSSNVGMTLLEQKMGDATWLDYLNRFKFGVPTRFGLTDEYAGQLPADN	441
Sbjct	301	G MMTF QGFAHSSNVGM+LLEQKMGDATWLDYL RFKFGVPTRFGLTDEYAGQLPADN	360
Query	442	IVNIAQSSFGQGQGIVTQTMIRAFTAIANDGVMLEPKFISAIYDPNDQTARKSQKEIVGN	501
Sbjct	361	IV+IAQSSFGQGIVTQTM+RAFTAIA ANDGVMLEPKFISAIYD N+Q+ RKSQKEIVGN	420
Query	502	PVSKDAASLRTNMVLVGTDPVYGTMYNHSTGKPTVTVPQONVALKSGTAQIADEKNGGY	561
Sbjct	421	PVSK+AAS TR +M+LVGTD+YGTMYNH TGKP +TVPGQNV+A KSGTAQIADEKNGGY	480
Query	562	LVGLTDYI FSAVSMSPAENPDFILYVTVQQPEHYSGIQLGEFANPILERASAMKDSLNLQ	621
Sbjct	481	LVG T+YIFS V+M+PAENPDFILYVTVQQPEHYSGIQLGEFA PILERASAMK+SLNLQ	540
Query	622	TTAKALEQVSQQSPYPMPSVKDISPGDLAEELRRLVQPIVVGTGKIKKNSSAEEGKNLA	681
Sbjct	541	+ AK L+ +V+ +S Y MPS+KDISPG+LAE LRRN+VQPIVVGTGKIK +S EEG NLA	600
Query	682	SPAKNLDKVTESSYAMPSIKDISPGELAEALRRNIVQPIVVGTGKIKETSVEEGTNLA	741
PNNQVLI LSDKAEEVPDMYGTWTKETAETLAKWLNLIELEFQGSGSTVQKQDVRAKTAIKDI			
PNNQVLI LSDK EE+PDGYGW KETAET AKWL+IELEF+GSGS VQKQDV NTAIK+I			

• Sbjct 601 PNQQVLLSDKVEEIPDMYGWKKETAETFAKWL DIELEFEGSGSVVQKQDVRTNTAIKNI 660
 Query 742 KKITLTLGD 750
 - Sbjct 661 KKIKLTLGD 669

>gb|AY56851.1| penicillin-binding protein 2X [Streptococcus pneumoniae]
 Length=668

Score = 1152 bits (2980), Expect = 0.0, Method: Composition-based stats.
 Identities = 593/668 (88%), Positives = 631/668 (94%), Gaps = 0/668 (0%)

Query 83	NGVPIAEDATSYNVYAVIDENYKSATGKILYVEKTQFNKVAEVFKYLDMEESYVREQLS	142
Sbjct 1	NGVPIAEDATSYNVYAVIDENYKSATGKILYVEKTQFNKVAEVFKYLDMEESYVREQLS	60
Query 143	QPNLKQVSFGAKGNIGITYANMMSIKKELEAAEVKGIDFTTSPNRSYPNGQFASSFIGLAQ	202
Sbjct 61	QPNLKQVSFG+KGNGITYANMMSIKKELE AEVKGIDFTTSPNRSYPNGQFASSFIGLAQ	120
Query 203	LHENEDGSKSLGTSGMESSLNSILAGTDGIITYEKDRLGNI VPGTEQVSQRTMDGKD VY	262
Sbjct 121	LHENEDGSKSLGTSGMESSLNSILAGTDGIITYEKDRVGNI VPGTELVSQQTVDGKD VY	180
Query 263	TTISSLPLQSFMETQMDAFQEKVKGKYM TATLVSAKTGEILATTQRPTFDADTKEGIT EDF	322
Sbjct 181	TTISSLPLQSFMETQMDAF EKVKGKYM TATLVSAKTGEILATTQRPTF+ADTKEGIT EDF	240
Query 323	VWRDILYQSNYEPGSTMKVMM LAAAIDNNTFPGGEVFNSELKIADATIRDWDVN EGLTG	382
Sbjct 241	VWRDILYQSNYEPGS MKVM LA++IDNNTFP GE FNSSE KIADAT RDWDVN+GLT	300
Query 383	GRMMTFSQGFAHSSNVGM TLEQKMGDATWLDYLNRKFVGPTRFGLTDEYAGQLPADNI	442
Sbjct 301	G MMFT QGFAHSSNVGM+LLEQKMGDATWLDYL RFKFGVPTRFGLTDEYAGQLPADNI	360
Query 443	GGMMTFLQGFAHSSNVGMSLLEQKMGDATWLDYLKRKFVGPTRFGLTDEYAGQLPADNI	
Sbjct 361	VNIAQSSFGQQGISVTQTMIRFTA IANDGVMLEPKFISAIYDPNDQTARKSQKEIVGNP	502
Sbjct 361	V+IAQSSFGQQGISVTQTM+RAFTA IANDGVMLEPKFISAIYD N+Q+ RKSQKEIVGNP	420
Sbjct 421	VSKEAASSTTRNHMILVGTDPYLTGMYNHTGKPIITVPGQNVAVKSGTAQIADEKNGGYL	562
Sbjct 421	VSKDAASLRTTNMVLVGTDPVYGT MYNHSTGKPTVTVPGQNVALKSGTAQIADEKNGGYL	480
Query 563	VSKEAASSTTRNHMILVGTDPYLTGMYNHTGKPIITVPGQNVAVKSGTAQIADEKNGGYL	
Sbjct 481	VGLTDYI FSAVSMSPAENPDFI LYVTVQOPEHYSGIQLGEFANPILERASAMKDSLNLQ	622
Sbjct 481	VG T+YIFS V+M+PAENPDFI LYVTVQOPEHYSGIQLGEFA PILERASAMK+SLNLQ+	540
Query 623	VGSTNYIFSVVTMNP AENPDFI LYVTVQOPEHYSGIQLGEFATPILERASAMKESLNQ	
Sbjct 541	TAKALEQVSSQSPYPMPSVKDISPGD LAEE LRRNLVQPI VVGTGKIKN SSAEEGKNLAP	682
Sbjct 541	AK L++V+ +S Y MPS+KDISPG+LAE LRRN+VQPI VVGTGKIK +S EEG NLAP	
Sbjct 541	PAKNLDKVTESSYAMPSIKDISPGELAEALRRNIVQPI VVGTGKIKETSVEEGTNLAP	600
Query 683	NQQVLI LSDKAEEV PDMYGW KETAETLAKWL NIELEFQGSGSTVQKQDVRANTAIKDIK	742
Sbjct 601	NQQVL+LSDK EE+PDMYGW KETAET AKWL+IELEF+GSGS VQKQDVR NTAIK+IK	
Sbjct 601	NQQVLLSDKVEEIPDMYGW KETAETFAKWL DIELEFEGSGSVVQKQDVRTNTAIKNI	660
Query 743	KITLTLGD 750	
Sbjct 661	KIKLTLGD 668	

>gb|AY56841.1| penicillin-binding protein 2X [Streptococcus pneumoniae]
 Length=674

Score = 1150 bits (2974), Expect = 0.0, Method: Composition-based stats.
 Identities = 592/674 (87%), Positives = 634/674 (94%), Gaps = 0/674 (0%)

Query 77	GTIYDRNGVPIAEDATSYNVYAVIDENYKSATGKILYVEKTQFNKVAEVFKYLDMEESY	136
Sbjct 1	GTIYDRNGVPIAEDATSYNVYAVID+ YKSATGKILYVE QFNKVAEVFKYLDM+E+Y	
Sbjct 1	GTIYDRNGVPIAEDATSYNVYAVIDKKYKSATGKILYVEDAQFNKVAEVFKYLDMDEAY	60
Query 137	VREQLSQPNLKQVSFGAKGNIGITYANMMSIKKELEAAEVKGIDFTTSPNRSYPNGQFASS	196
Sbjct 61	V+EQLSQPNL QVSFGAKGNIGITYANMM+IKK+L+ A ++GIDFTTSPNRSYPNGQFASS	
Sbjct 61	VKEQLSQPNLTQVSFGAKGNIGITYANMMAIKKDLKDASIEGIDFTTSPNRSYPNGQFASS	120
Query 197	FIGLAQLHENEDGSKSLGTSGMESSLNSILAGTDGIITYEKDRLGNI VPGTEQVSQRTM	256
Sbjct 121	FIGLAQLHENEDGSKSLGTSGMESSLNSILAG DGIITYEKDRLGNI VPGTEQVSQ+T+	
Sbjct 121	FIGLAQLHENEDGSKSLGTSGMESSLNSILAGKDGIITYEKDRLGNI VPGTEQVSQQT	180
Query 257	DGKDVTI SSPLQSFMETQMDAFQE KVKGKYM TATLVSAKTGEILATTQRPTFDADTK	316
Sbjct 181	DGKDVTI SSPLQSFMETQMDAF+AF EKVKGKYM TATLVSAKTGEILATTQRPTF+ADTK	
Sbjct 181	DGKDVTI SSPLQSFMETQMDAF EKVKGKYM TATLVSAKTGEILATTQRPTFNADTK	240
Query 317	GITEDFWRDILYQSNYEPGSTMKVMM LAAAIDNNTFPGGEVFNSELKIADATIRDWDV	376
	GITEDFWRDILYQSNYEPGS MKVM LA++IDNNTFP GE FNSSE KIADAT RDWDV	

Sbjct	241	GITEDFVWRDILYQSNYEPGSAMKVMLASSIDNNTFPSGEYFNSSEFKIADATTRDWDV	300
Query	377	NEGLTGGGRMMTFSQGFAHSSNVGMTLLEQKMGDATWLDYLNRFKFGVPTRFGLTDEYAGQ N+GLT G MMTF QGFAHSSNVGM+LLEQKMGDATWLDYL RFKFGVPTRFGLTDEYAGQ	436
Sbjct	301	NDGLTTGGMMTFLQGFAHSSNVGMSLLEQKMGDATWLDYLKRFKFGVPTRFGLTDEYAGQ	360
Query	437	LPADNIVNIAQSSFGQGI SVTQTQMIRAFTAIANDGVMLEPKFISAIYDPNDQTARKSQQ LPADNIV+IAQSSFGQGI SVTQTQM+RAFTAIANDGVMLEPKFISAIYD N+Q+ RKSQQ	496
Sbjct	361	LPADNIVSIAQSSFGQGI SVTQTQMIRAFTAIANDGVMLEPKFISAIYDTNNQSVRKSQQ	420
Query	497	EIVGNPVSKEAASSTTRNHMILVGTDPYGTMYNHTGKPIITVPGQNVAVKSGTAQIADE EIVGNPVS+AAAS TR +M+LVGTD+YGTMYNH TGKP +TVPGQNVVA+KSGTAQIADE	556
Sbjct	421	EIVGNPVSKEAASSTTRNHMILVGTDPYGTMYNHTGKPIITVPGQNVAVKSGTAQIADE	480
Query	557	KNGGYLVLGTDYIFSAVSMSPAENPDFILYVTVQQPEHYSGIQLGEFANPILERASAMKD KNGGYLVG T+YIFS V+M+PAENPDFILYVTVQQPEHYSGIQLGEFA PILERASAMK+	616
Sbjct	481	KNGGYLVLGSTNYIFSVVTMNPNAENPDFILYVTVQQPEHYSGIQLGEFATPILERASAMKE	540
Query	617	SLNLQTTAKALEQVSQOSPYPMPSVKDISPGDLAEELRRNLVQPIVVGTGKIKNSSAEE SLNLQ+ AK L++V+ +S Y MPS+KDISPG+LAE LRRN+VQPIVVGTGKIK +S EE	676
Sbjct	541	SLNLQSPAKNLDKVTESSYAMPSIKDISPGELAEALRRNIVQPIVVGTGKIKETSVEE	600
Query	677	GKNLAPNQQVLILSDKAEEVPDMYGTKEAETLAKWLNIELEFQGSGSTVQKQDVRANT G NLAPNQQVLILSDKAEEVPDMYGTKEAETLAKWLNIELEF+GSGS VQKQDVR NT	736
Sbjct	601	GTNLAPNQQVLILSDKAEEVPDMYGTKEAETLAKWLNIELEFEGSGSVVQKQDVRTNT	660
Query	737	AIKDIKKITLTLGD 750	
Sbjct	661	AIKNIKKIKLTLGD 674	

>emb|CAA88920.1| penicillin-binding protein 2x [Streptococcus pneumoniae]
Length=666

Score = 1149 bits (2973), Expect = 0.0, Method: Composition-based stats.
Identities = 592/666 (88%), Positives = 628/666 (94%), Gaps = 0/666 (0%)

Query	85	VPIAEDATSYNVAVIDENYSATGKILYVEKTQFNKVAEVFKYLDMEESYVREQLSQP	144
Sbjct	1	VPIAEDATSYNVAVIDENYSATGKILYVEKTQFNKVAEVFKYLDMEESYVREQLSQP	60
Query	145	NLKQVSGAKGNGITYANMMSIKKELEAAEVKGIDFTTSPNRSPNGQFASSFIGLAQLH	204
Sbjct	61	NLKQVSGAKGNGITYANMM+IKKELE AEVKGIDFTTSPNRSPNGQFASSFIGLAQLH	120
Query	205	ENEDGSKSLLGTSGMESSLNSILAGTDGIIITYEKDRQLGNIVPGTEQVSORTMDGKDVTYTT	264
Sbjct	121	ENEDGSKSLLGTSGMESSLNSILAGTDGIIITYEKDRQLGNIVPGTE VSQ+T+DGKDVTYTT	180
Query	265	ISSPLQSFMETQMDAQEVKVKGKYMTATLVSAKTGEILATTQRPTFDADTKEGITEDFVW +SSPLQSFMETQMDAF EKVKGKYMTATLVSAKTGEILATTQRPTF+ADTKEGITEDFVW	324
Sbjct	181	LSSPLQSFMETQMDAFLEKVKGKYMTATLVSAKTGEILATTQRPTFNADTKEGITEDFVW	240
Query	325	RDILYQSNYEPGSTMVMMMLAAAIDNNTFPGGEVFNSSELKIADATIRDWDVNNEGLTGGR	384
Sbjct	241	RDILYQSNYEPGS KVMMMA++IDNNTFP GE FNSSE KIADAT RDWDVNNEGLTGGR	300
Query	385	MMTFSQGFAHSSNVGMTLLEQKMGDATWLDYLNRFKFGVPTRFGLTDEYAGQLPADNIVN	444
Sbjct	301	MMTFSQGFAHSSNVG+LLEQKMGDATWLDYL RFKFGVPTRFGLTDEYAGQLPADNIV+ MMTFSQGFAHSSNVGTSLLQKMGDATWLDYLKRFKFGVPTRFGLTDEYAGQLPADNIVS	360
Query	445	IAQSSFGQGI SVTQTQMIRAFTAIANDGVMLEPKFISAIYDPNDQTARKSQQEIVGNPVS	504
Sbjct	361	IAQSSFGQGI SVTQTQM+RAFTAIANDGVMLEPKFISAIYD N+Q+ RKSQQEIVGNPVS	420
Query	505	KDAASLRTNMVLVGTDPVYGTMYNHSTGKPTVTPGQNVALKSGTAQIADEKNGGYLVG	564
Sbjct	421	KEAASSTTRNHMILVGTDPYGTMYNHTGKPIITVPGQNVAVKSGAAQIADEKNGGYLVG	480
Query	565	LTDYIFSAVSMSPAENPDFILYVTVQQPEHYSGIQLGEFANPILERASAMKDSLNLQTTA T+YIFS V+M+PAENPDFILYVTVQQPEHYSGIQLGEFA PILERASAMK+SLNLQ+ A	624
Sbjct	481	STNYIFSVVTMNPNAENPDFILYVTVQQPEHYSGIQLGEFATPILERASAMKESLNQSPA	540
Query	625	KALEQVSQQSPYPMPSVKDISPGDLAEELRRNLVQPIVVGTGKIKNSSAEGKNLAPNQ	684
Sbjct	541	KNLKVTESSYAMPSIKDISPGELAEALRRNIVQPIVVGTGKIKETSVEEGTNLAPNQ	600
Query	685	QVLILSDKAAEEVPDMYGTKEAETLAKWLNIELEFQGSGSTVQKQDVRANTAIKDIKKI	744
Sbjct	601	QVLILSDKVEEIPDMYGW KETAET AKWL+IELEF+GSGS VQKQDVR NTAIK+IKKI	660
Query	745	TLTGKD 750	
Sbjct	661	KLTLGD 666	

>emb|CAA88919.1| penicillin-binding protein 2x [Streptococcus pneumoniae]
Length=666

Score = 1149 bits (2971), Expect = 0.0, Method: Composition-based stats.
Identities = 592/666 (88%), Positives = 628/666 (94%), Gaps = 0/666 (0%)

Query	85	VPIAEDATSYNVAVIDENYKSATGKILYVEKTQFNKVAEVFKYLDMEESYVREQLSQP	144
Sbjct	1	VPIAEDATSYNVAVIDENYKSATGKILYVEKTQFNKVAEVFKYLDMEESYVREQLSQP	60
Query	145	NLKQVSFGAKGNGITYANMMSIKKELEAAEVKGIDFTTSPNRSPNGQFASSFIGLAQLH	204
Sbjct	61	NLKQVSFGAKGNGITYANMM+IKKELE AEVKGIDFTTSPNRSPNGQFASSFIGLAQLH	120
Query	205	ENEDGSKSLLGTSMESSLNSILAGTDGIITYEKDRGNIVPGTEQVSQRTMDGKDVTYTT	264
Sbjct	121	ENEDGSKSLLGTSMESSLNSILAGTDGIITYEKDRGNIVPGTE VSQ+T+DGKDVTYTT	180
Query	265	ISSLPLQSFMETQMDAFQEVKVGKYMATTLSAKTGEILATTQRPTFDADTKEGITEDFVW	324
Sbjct	181	+SSPLQSFMETQMDAF EKVVGKYMATTLSAKTGEILATTQRPTF+ADTKEGITEDFVW	240
Query	325	RDILYQSNYEPGSTMVKVMMIAAAIDNNTFPGGEVFNSELKIADATIRDWDVNNEGLTGGR	384
Sbjct	241	RDILYQSNYEPGS KVMMIA++IDNNTFP GE FNSSE KIADAT RDWDVNNEGLTGGR	300
Query	385	MMTFSQGFAHSSNVGMTLLEQKMGDATWLDYLNRFKFGVPTRFGLTDEYAGQLPADNIVN	444
Sbjct	301	MMTFSQGFAHSSNVVG +LLEQKMGDATWLDYL RFKFGVPTRFGLTDEYAGQLPADNIV+	360
Query	445	IAQSSFGQGIVTQTQMIRAFTAIANDGVMLEPKFISAIYDPNDQTARKSQKEIVGNPVS	504
Sbjct	361	IAQSSFGQGIVTQTQMLRAFTAIANDGVMLEPKFISAIYDTNNQSVRSQKEIVGNPVS	420
Query	505	KDAASLTTRNMVLVGTDPVYGTMYNHSTGKPTVTVPQONVALSGTAQIADEKNGGYLVG	564
Sbjct	421	KEAASSTRNHHMILVGTDPYGTMYNHGTKPIITVPGQNAVKGTAQIADEKNGGYLVG	480
Query	565	LTDYIFSAVSMSPAENPDFILYVTVQQPEHYSGIQLGEFANPILERASAMKDSLNLQTTA	624
Sbjct	481	T+YIFS V+M+PAENPDFILYVTVQQPEHYSGIQLGEFA PILERASAMK+SLNLQ+ A	540
Query	625	STNYIFSVVTMNPAPAENPDFILYVTVQQPEHYSGIQLGEFATPILERASAMKESLNQSPA	600
Sbjct	541	KALEQVSOQSPYPMPSVKDISPGDLAEELRRNLVQPIIVVGTGTKIKNSSAEEGKNLAPNQ	684
Sbjct		K L++V+ +S Y MPS+KDISPG+LAE LRRN+VQPIIVVGTGTKIK +S EEG NLAPNQ	
Sbjct		KNLDKVTESSYAMPSIKDISPGELAEALRRNIVQPIIVVGTGTKIKETSVEEGTNLAPNQ	
Query	685	QVLILSDKAAEVPDMYWTKETAETLAKWLNIELEFQGSGSTVQKQDVRANTAIKDIKKI	744
Sbjct	601	QVL+LSDK EE+PDMD W KETAET AKWL+IELEF+GSGS VQKQDVR NTAIK+IKKI	660
Query	745	QVLLLSDKVEEIPDMYSWKETAETFAKWL DIELEFEGSGS VVQKQDVRTNTAIKNIKKI	
Sbjct	661	QVLLLSDKVEEIPDMYSWKETAETFAKWL DIELEFEGSGS VVQKQDVRTNTAIKNIKKI	
Query	745	TLTLGD 750	
Sbjct	661	TLTLGD 666	

>emb|CAB65448.1| penicillin binding protein 2x [Streptococcus pneumoniae]
Length=666

Score = 1148 bits (2970), Expect = 0.0, Method: Composition-based stats.
Identities = 594/666 (89%), Positives = 627/666 (94%), Gaps = 0/666 (0%)

Query	85	VPIAEDATSYNVAVIDENYKSATGKILYVEKTQFNKVAEVFKYLDMEESYVREQLSQP	144
Sbjct	1	VPIAEDATSYNVAVIDENYKSATGKILYVEKTQFNKVAEVFKYLDMEESYVREQLSQP	60
Query	145	NLKQVSFGAKGNGITYANMMSIKKELEAAEVKGIDFTTSPNRSPNGQFASSFIGLAQLH	204
Sbjct	61	NLKQVSFGAKGNGITYANMM+IKKELE AEVKGIDFTTSPNRSPNGQFASSFIGLAQLH	120
Query	205	ENEDGSKSLLGTSMESSLNSILAGTDGIITYEKDRGNIVPGTEQVSQRTMDGKDVTYTT	264
Sbjct	121	ENEDGSKSLLGTSMESSLNSILAGTDGIITYEKDRGNIVPGTE VSQ+T+DGKDVTYTT	180
Query	265	ISSPLQSFMETQMDAFQEVKVGKYMATTLSAKTGEILATTQRPTFDADTKEGITEDFVW	324
Sbjct	181	ISSSTLQSFMETQMDAF EKVVGKYMATTLSAKTGEILATTQRPTF+ADTKEGIT+DFVW	240
Query	325	RDILYQSNYEPGSTMVKVMMIAAAIDNNTFPGGEVFNSELKIADATIRDWDVNNEGLTGGR	384
Sbjct	241	RDILYQSNYEPGS MKVM LAAAIDNNTFP GE FNSSE KIADAT RDWDVN GLT G	300
Query	385	MMTFSQGFAHSSNVGMTLLEQKMGDATWLDYLNRFKFGVPTRFGLTDEYAGQLPADNIVN	444
Sbjct	301	MMTFLQGFAHSSNVGMSLLEQKMGDATWLDYLKRFKFGVPTRFGLTDEYAGQLPADNIVS	360
Query	445	IAQSSFGQGIVTQTQMIRAFTAIANDGVMLEPKFISAIYDPNDQTARKSQKEIVGNPVS	504

Sbjct	361	IAQSSFGQQGISVTQTQM+RA TAIANDGVMLEPKFISAIYD N+N+ RKSQKEIVGNPVS IAQSSFGQQGISVTQTQMLRALTAIANDGVMLEPKFISAIYDTNNQSVRKSQKEIVGNPVS	420
Query	505	KDAASLRTNMVLVGTDPVYGTMYNHSTGKPTVTVPQONVALKSGTAQIADEKNGGYLVG K+AAS TR +M+LVGTD+YGTMYNH TGKP +TVPGQNV+A+KSGTAQIADEKNGGYLVG	564
Sbjct	421	KEAASSTTRNHHMILVGTDPFLYGTMYNHGTKPIITVPGQNVAVKSGTAQIADEKNGGYLVG	480
Query	565	LTDYIFSAVMSPAENPDFILYVTVQQPEHYSGIQLGEFANPILERASAMKDSLNLQTTA T+YIFS V+M+PAENPDFILYVTVQQPEHYSGIQLGEFA PILERASAMK+SLNLQ+ A	624
Sbjct	481	STNYIFSVVTMNPNAENPDFILYVTVQQPEHYSGIQLGEFATPILERASAMKESLNLQSPA	540
Query	625	KALEQVSSQQSPYPMPSVKDISPGDLAEELRRNLVQPIVVGTVGTKIKKNSSAEEGKNLAPNQ K L++V+ +S Y MPS+KDISPG+LAE LRRN+VQPIVVGTVGTKIK +S EEG NLAPNQ	684
Sbjct	541	KNLDKVTESSYAMPSIKDISPGELAEALRRNIVQPIVVGTVGTKIKETSVEEGTNLAPNQ	600
Query	685	QVLILSDKAAEVPDMYGTWTKETAETLAKWLNLIEFQGSGSTVQKQDVRVANTAIKDIKKI QVL+LSDK EE+PDMYGW KETAET AKWL+IELEF+GSGS VQKQDVR NTAIK+IKKI	744
Sbjct	601	QVLLLSDKVVEIPDMYGWKKETAETFAKWL DIELEFEGSGS VVQKQDVRNTAIKNIKKI	660
Query	745	TTLGD 750	
Sbjct	661	KTLGD 666	

>emb|CAA67012.1| penicillin-binding protein [Streptococcus pneumoniae]
Length=666

Score = 1148 bits (2970), Expect = 0.0, Method: Composition-based stats.
Identities = 590/666 (88%), Positives = 631/666 (94%), Gaps = 0/666 (0%)

Query	85	VPIAEDATS NVYAVIDENYKSATGKILYVEKTQFNKVAEVFHKYLDMEESYVREQLSQP VPIAEDATS NVYAVID+ YKSATGKILYVE +QFNKVAEVFHKYLDM+E+YV+EQL+QP	144
Sbjct	1	VPIAEDATS NVYAVIDK KYKSATGKILYVEDSQFNKVAEVFHKYLDMDEAYVKEQLAQ	60
Query	145	NLKQVSGAKGNGITYANMMSIKKELEAAEVKGIDFTTSPNRSYPNGQFASSFIGLAQLH NL QVSFGAK NGITYANMM+IKK+L+ A V+GIDFTTSPNRSYPNGQFASSFIGLAQLH	204
Sbjct	61	NLTQVSGAKENGITYANMMAIKKDLKDASVEGIDFTTSPNRSYPNGQFASSFIGLAQLH	120
Query	205	ENEDGSKSLLG TSGMESSLNSILAGTDGIITYEKDRRLGNIVPGTEQVSQRTMDGKD VYTT ENEDGSKSLLG T G+ESSLN+ILAGTDGIITYEKDR+GNIVPGTE VSQ+T+DGKD VYTT	264
Sbjct	121	ENEDGSKSLLG TFGLESSLNTILAGTDGIITYEKDRVGNIVPGTELVSQQTVDGKD VYTT	180
Query	265	ISSPLQS FMETQMDAFQE KVKGKYM TATLVS AKTGEILATTQRPTFDADTKEGITEDFVW +SSPLQS FMETQMDAF EKVKGKYM TATLVS AKTGEILATTQRPTF+ADTK+GIT+DFVW	324
Sbjct	181	LSSPLQS FMETQMDAF LEKVKGKYM TATLVS AKTGEILATTQRPTFNADTKDG ITKDFVW	240
Query	325	RDILYQSNYEPGSTMVKVMM LAAAIDDNNTFPGEVFNSSELKIA DATIR DWVNEGLTGGR RDILYQ NYEPGS MKVM LA++IDDNNTFPGE FNSSE KIA D T RD DWVNEGLTG	384
Sbjct	241	RDILYQGNYEPGSAMKVMTLASSIDDNNTFPGEY FNSSES KIA DVTR DWVNEGLTGG	300
Query	385	MMTFSQGFAHSSNVGM TLEQKMGDATWLDYLNRFKFGV PTRFGLTDEYAGQLPADNIVN MMTFSQGFAHSSNVGM LLE+KMGD TWLDYLNRFKFGV PTRFGLTDEYAGQLPADNIV+	444
Sbjct	301	MMTFSQGFAHSSNVGM ILL EKMGDTT WLDYLNRFKFGV PTRFGLTDEYAGQLPADNIVS	360
Query	445	IAQSSFGQQGISVTQTQMIRAF TAI ANDGVMLEPKFISAIYDPNDQTARKS QKEIVGNPVS IAQSSFGQQGISVTQTQMIRAF TAI ANDGVMLEPKF -A+YDPNDQT RKSQKEIVGNPVS	504
Sbjct	361	IAQSSFGQQGISVTQTQMIRAF TAI ANDGVMLEPKFITALYDPNDQTVRKS QKEIVGNPVS	420
Query	505	KDAASLRTNMVLVGTDPVYGTMYNHSTGKPTVTVPQONVALKSGTAQIADEKNGGYLVG KDAAS TRT MVLVGTDPVYGTMYNHSTGKP VTVPQONVALKSGTAQIADEKNGGYLVG	564
Sbjct	421	KDAASQTRTQMVLVGTDPVYGTMYNHSTGKP I VTVPGQNVALKSGTAQIADEKNGGYLVG	480
Query	565	LTDYIFSAVMSPAENPDFILYVTVQQPEHYSGIQLGEFANPILERASAMKDSLNLQTTA T+YIFS ++++PAENPDFILYVTVQQPEHYSGIQLGEFA PILERASAMK+SL LQ+ A	624
Sbjct	481	STNYIFSLLTINPAENPDFILYVTVQQPEHYSGIQLGEFATPILERASAMKESLYLQSPA	540
Query	625	KALEQVSSQQSPYPMPSVKDISPGDLAEELRRNLVQPIVVGTVGTKIKKNSSAEEGKNLAPNQ K L++V+ +S Y MPS+KDISPGDLAEELRRN+VQPIVVGTVGTKIK SS EEG+NL+PNQ	684
Sbjct	541	KNLDKVTESSYAMPSIKDISPGDLAEELRRNIVQPIVVGTVGTKIK ESS VEEGRNLSPNQ	600
Query	685	QVLILSDKAAEVPDMYGTWTKETAETLAKWLNLIEFQGSGSTVQKQDVRVANTAIKDIKKI QVLILSDKAAEVPDMYGTWTKETAET AKWLNLIEF+GSGSTVQKQDVRVANTAIKDIKKI	744
Sbjct	601	QVLILSDKAAEVPDMYGTWTKETAETFAKWLNLIEFEGSGSTVQKQDVRVANTAIKDIKKI	660
Query	745	TTLGD 750	
Sbjct	661	TTLGD 666	

>emb|CAA67010.1| penicillin-binding protein [Streptococcus pneumoniae]
Length=666

Score = 1146 bits (2964), Expect = 0.0, Method: Composition-based stats.
Identities = 586/666 (87%), Positives = 631/666 (94%), Gaps = 0/666 (0%)

Query 85 VPIAEDATS NVYAVIDENYKSATGKILYVEKTQFNKVAEVFHKYLDMEESYVREQLSQP 144

Sbjct	1	VPIAEDATSYNVAVID+ YKSATGKILYVE +QFNKVAEVFKYLDM+E+YV+EQL+QP VPIAEDATSYNVAVIDKKYKSATGKILYVEDSQFNKVAEVFKYLDMDEAYVKEQLAQP	60
Query	145	NLKQVSFGAKGNGITYANMMSIKKELEAAEVKGIDFTTSPNRSPNGQFASSFIGLAQLH NL QVSFGAKGNGITYANMM+IKK+L+ A V+GIDFTTSPNRSPNGQFASSFIGLAQLH	204
Sbjct	61	NLTQVSFGAKGNGITYANMMAIKKDLKDASVEGIDFTTSPNRSPNGQFASSFIGLAQLH	120
Query	205	ENEDGSKSLLGTSGMESSLNSILAGTDGI ITYEKDRILGNIVPGTEQVSQRTMDGKDVT ENEDGSKSLLGT G+ESSLN+ ILAGTDGI ITYEKD +GNIVPGTE VSQ+T+DGKDVT ENEDGSKSLLGTGLESSLNTILAGTDGI ITYEKDGVGNIIVPGTELVSQQTVDGKDVT	264
Sbjct	121	ENEDGSKSLLGTGLESSLNTILAGTDGI ITYEKDGVGNIIVPGTELVSQQTVDGKDVT	180
Query	265	ISSPLQSFMETQMDAFQEKVKKGKYMTATLVSAKTGEILATTQRPTFDADTKEGITEDFW +SSPLQSFMETQMDAF +KVKGKYMTATLVSAKTGEILATTQRPTF+ADTKEGITEDFW	324
Sbjct	181	LSSPLQSFMETQMDAFLQKVKGKYMTATLVSAKTGEILATTQRPTFNADTKEGITEDFW	240
Query	325	RDILYQSNYPEGSTMVKVMMIAAAIDNNTFPGGEVNSSELKIADATIRDWDVNNEGLTGG RDILYQ NYEPGS MKVM LA++IDNNTFPGGE FNSSE KIAD T RDWDVNNEGLTGG	384
Sbjct	241	RDILYQGNYEPGSAMKVMTLASSIDNNTFPGGEYFNSSESKIADVTTRDWDVNNEGLTGGG	300
Query	385	MMTFSQGFAHSSNVGMTLLEOKMGDATWLDPYLNRFKFGVPTRFGLTDEYAGQLPADNIVN MMTFSQGFAHSSNVGM LLE+KMGD TWLDYLNRFKFGVPTRFGLTDEYAGQLPADNIV+	444
Sbjct	301	MMTFSQGFAHSSNVGMILLEEKMGDTTWLDYLNRFKFGVPTRFGLTDEYAGQLPADNIVS	360
Query	445	IAQSSFGQGISVTQTQMIRAFATAIANDGVMLEPKFISAIYDPNDQTARKSQKEIVGNPVS IAQSSFGQGISVTQTQM+RAFTAIA ANDGVMLEPKFISAIYD N+Q+ RKSQKEIVG PVS	504
Sbjct	361	IAQSSFGQGISVTQTQMLRAFTAIANDGVMLEPKFISAIYDTNNQSVRSQKEIVGKPVS	420
Query	505	KDAASLTRTNMVLVGTDPVYGTMYNHSTGKPTVTVPQNVALKSGTAQIADEKNGGYLVG +DAASLTRTNM+LVGTDP+YGTMYNH TGKP +TVPGQNVA+KSGTAQIADEKNGGYLVG	564
Sbjct	421	EDAASLTRTNMILVGTDPYGTMYNHQTGKPIITVPGQNVAVKSGTAQIADEKNGGYLVG	480
Query	565	LTDYIFSAVSMSPAENPDFILYVTVQQPEHYSGIQLGEFANPILERASAMKDSLNLQTTA T+YIFS V+M+PAENPDFILYVTVQQPEH+SGIQLGEFANPILERASAMK+SLNLQ+ A	624
Sbjct	481	STNYIFSVVTMNPAAENPDFILYVTVQQPEHFSGIQLGEFANPILERASAMKESLNLQSPA	540
Query	625	KALEQVSSQSPYPMPSVKDISPGDLAEEELRRNLVQPIVVGTTKIKKNSSAEEGKNLAPNQ K L+QVS Q+ Y MPS+K+ISPGDLAEEELRRN+VQPIVVGTTKIK SS EEG+NL+PNQ	684
Sbjct	541	KNLDQVSSQTSYAMPSIKNISPGDLAEEELRRNIVQPIVVGTTKIKKESSEEEGRNLSPNQ	600
Query	685	QVLILSDKAEEVPDMYGTWTKETAETLAKWLNIELEFQGSGSTVQKQDVRANTAIKDIKKI QVLILSDKAEEVPDMYGTWTKETAET AKWLNIELEF+GSGSTVQKQDVRANTAIKDIKKI	744
Sbjct	601	QVLILSDKAEEVPDMYGTWTKETAETFAKWLNIELEFEGSGSTVQKQDVRANTAIKDIKKI	660
Query	745	TLTLGD 750 +TLGD	
Sbjct	661	YITLGD 666	

>gb|AYY56856.1| penicillin-binding protein 2X [Streptococcus pneumoniae]
Length=669

Score = 1145 bits (2961), Expect = 0.0, Method: Composition-based stats.
Identities = 587/669 (87%), Positives = 628/669 (93%), Gaps = 0/669 (0%)

Query	82	RNGVPIAEDATSYNVAVIDENYKSATGKILYVEKTQFNKVAEVFHKYLDMEESYVREQL RNGVPIAEDATSYNVAVID+ YKSATGKILYVE QFNKVAEVFHKYLDM+E+YV+EQL	141
Sbjct	1	RNGVPIAEDATSYNVAVIDKKYKSATGKILYVEDAQFNKVAEVFHKYLDMDEAYVKEQL	60
Query	142	SOPNLKOVSFGAKGNGITYANMMSIKKELEAAEVKGIDFTTSPNRSPNGQFASSFIGLA SQPNL QVSFGAKGNGITYANMM+IKKELE AEVKGIDFTTSPNRSPNGQFASSFIGLA	201
Sbjct	61	SQPNLTQVSFGAKGNGITYANMMAIKKELETAEVKGIDFTTSPNRSPNGQFASSFIGLA	120
Query	202	OLHENEDGSKSLLGTSGMESSLNSILAGTDGIITYEKDRLGNIVPGTEQVSQRTMDGKDV OLHENEDGSKSLLGTSGMESSLNSILAG DGIITYEKDRLGNIVPGTEQVSQ+T+DGKDV	261
Sbjct	121	OLHENEDGSKSLLGTSGMESSLNSILAGKDGIITYEKDRLGNIVPGTEQVSQQTVDGKDV	180
Query	262	YTTISSLQSFMETQMDAFQEVKVGKYMATTLSAKTGEILATTQRPTFDADTKEGITED YTT+SSPLQSFMETQMDAF EKVVGKYMATTLSAKTGEILATTQRPTF+ADTKEGITED	321
Sbjct	181	YTTLSSPLQSFMETQMDAFLEKVKVGKYMATTLSAKTGEILATTQRPTFNADTKEGITED	240
Query	322	FVWRDILYQSNYEPMSTMKVMMIAAAIDNNTFPGGEVFNSSELKIADATIRDWDVNNEGLT FVWRDILYQSNYEPMG MKVM LA++IDNNTFP GE FNSSE KIADAT RDWDVN+GLT	381
Sbjct	241	FVWRDILYQSNYEPMGAMKVMTLASSIDNNTFPSGEYFNSSEFKIADATTRDWDVNNDGLT	300
Query	382	GGRMMTFSQGFAHSSNVGMTLLEQKMGDATWLDYLNRFKFGVPTRFGLTDEYAGQLPADN G MMTF QGFAHSSNVGM+LLEQKMGDATWLDYL RFKFGVPTRFGLTDEYAGQLPADN	441
Sbjct	301	TGGMMTFLQGFAHSSNVGMSLLEQKMGDATWLDYLKRFKFGVPTRFGLTDEYAGQLPADN	360
Query	442	IVNIAQSSFGQGISVTQTMIRFTAIAANDGVMLEPKFISAIYDPNDQTARKSQKEIVGN IV+IAQSSFGQGISVTQTM+RAFTAIAANDGVMLEPKFISAIYD N+Q+ RKSQKEIVGN	501
Sbjct	361	IVSIAQSSFGQGISVTQMLRAFTIAIAANDGVMLEPKFISAIYDTNNQSVRSQKEIVGN	420
Query	502	PVSKDAASLTRTNMVLVGTDPVYGTMYNHSTGKPTVTVPQONVALKSGTAQIADEKNGGY PVSK+AAS TR +M+LVGTDPM+YGTMYNH TGKP +TVPGQNVAVKSGTAQIADEKNGGY	561
Sbjct	421	PVSKEAASSTTRNHMILVGTDPYGTMYNHYTGKPI TVPGQNVAVKSGTAQIADEKNGGY	480

Query	562	LVGLTDYIFSAVSMSPAENPDFILYVTVQQPEHYSIGIQLGEFANPILERASAMKDSLNLQ	621
Lvg	T+YIFS V+M+PAENPDFILYVTVQQPEHYSIGIQLGEFA PILERASAMK+SLNLQ		
Sbjct	481	LVGSTNYIFSVVTMNPAAEPDFILYVTVQQPEHYSIGIQLGEFATPILERASAMKESLNQ	540
Query	622	TTAKALEQVSQQSPYPPMPSVKDISPGDLAEELRRNLVQPIIVVGTGKIKNNSAEEGKNLA	681
+ AK L++V+ +S Y MPS+KDISPG+LAE LRRN+VQPIIVVGTGKIK +S EEG NLA			
Sbjct	541	SPAKNLDKVTESSYAMPSIKDISPGELAEALRRNIVQPIIVVGTGKIKETSVEEGTNLA	600
Query	682	PNQQVLILSDKAEEVPDMYGWTKETAETLAKWLNIIELEFQGSGSTVQKQDVRANTAIKDI	741
PNQQVL+LSDK EE+PDMDYGW KETAET AKWL+IELEF+GSGS VQKQDVR NTAIK+I			
Sbjct	601	PNQQVLLLSDKVEEIPDMYWGKKETAETFAKWLDIELEFEGSGSVVQKQDVRTNTAIKNI	660
Query	742	KKITLTLGD 750	
KKI LTLGD			
Sbjct	661	KKIKLTLGD 669	

>gb|AAN32864.1| penicillin-binding protein 2X [Streptococcus pneumoniae]
Length=661

Score = 1143 bits (2956), Expect = 0.0, Method: Composition-based stats. Identities = 588/661 (88%), Positives = 625/661 (94%), Gaps = 0/661 (0%)			
Query	90	DATSYNVYAVIDENYKSATGKILYVEKTQFNKVAEVFKYLDMEESYVREQLSQPNLKQV	149
Sbjct	1	DATSYNVYAVIDENYKSATGKILYVEKTQFNKVAEVFKYLDMEESYVREQLSQPNLKQV	60
Query	150	SFGAKGNIGINYANMMSIKKELEAAEVKGIDFTTSPNRSYPNGQFASSFIGLAQLHENEDG	209
Sbjct	61	SFGAKGNIGINYANMM+IKKELE AEVKGIDFTTSPNRSYPNGQFASSFIGLAQLHENEDG	120
Query	210	SKSLLGTSGMESSLNSILAGTDGIITYEKDRLGNIVPGTEQVSQRTMDGKDVTYTISSPL	269
Sbjct	121	SKSLLGTSGMESSLNSILAGTDGIITYEKDRLGNIVPGTEQVSQQTVDGKDVTYTISSPL	180
Query	270	QSFMETQMDAFQEKVKGKYMATTLSAKTGEILATTQRPTFDADTKEGITEDFWRDILY	329
Sbjct	181	QSFMETQM+AFQEKVKGKYMATTLSAKTGEILATTQRPTFDADTKEGLTDFWRDILY	240
Query	330	QSNYEPGSTMVKVMMIAAAIDNNTFPGGEVNSSELKIADATIRDWDVNNEGTLGGRRMMTFS	389
Sbjct	241	QSNYEPGS MKVM LA++IDNNTFP GE FNSSE KIADAT RDWDVN GLT G MMTF	300
Query	390	QGFAHSSNVGM+LLEQKMGDATWLDYLNRFKFGVPTRFGLTDEYAGQLPADNIVNIAQSS	449
Sbjct	301	QGFAHSSNVGM+LLEQKMGDATWLDYL RFKFGVPTRFGLTDEYAGQLPADNIV+IAQSS	360
Query	450	FGQGISVTQTMIRAFATAIANDGVMLEPKFISAIYDPNDQTARKSQKEIVGNPVSKDAAS	509
Sbjct	361	FGQGISVTQTM+RAFTAIAANDGVMLEPKFISAIYD N+Q+ RKSQKEIVGNPVSK+AAS	420
Query	510	LTRTNMVLVGTDPVYGTMYNHSTGKPTVTVPQONVALKSGTAQIADEKNGGYLVGLTDYI	569
Sbjct	421	TR +M+LVGTDP+YGTMYNH TGKP +TVPGQNV+KSGTAQIADEKNGGYLVG T+YI	480
Query	570	TTRNHMILVGTDPLYGTMYNHGTGKPIITVPGQNVAVKSGTAQIADEKNGGYLVGSTNYI	
Sbjct	481	FSAVSMSPAENPDFILYVTVQQPEHYSIGIQLGEFANPILERASAMKDSLNLQTTAKALEQ	629
Sbjct	481	FSVVTMNPAAEPDFILYVTVQQPEHYSIGIQLGEFATPILERASAMKESLNQSPAKNLDK	540
Query	630	VSQQSPYPPMPSVKDISPGDLAEELRRNLVQPIIVVGTGKIKNNSAEEGKNLAPNQQVLIL	689
Sbjct	541	V+ +S Y MPS+KDISPG+LAE LRRN+VQPIIVVGTGKIK +S EEGKNLAPNQQVL+L	
Sbjct	541	VTTESSYAMPSIKDISPGELAEALRRNIVQPIIVVGTGKIKETSVEEGKNLAPNQQVLL	600
Query	690	VSQSPYPPMPSVKDISPGDLAEELRRNLVQPIIVVGTGKIKNNSAEEGKNLAPNQQVLIL	749
Sbjct	601	SDKEE+PDMDYGW KETAET AKWL+IELEF+GSGS VQKQDVR NTAIK+IKKI LTG	
Sbjct	601	SDKVEEIPDMYWKETAEAFAKWLDIELEFEGSGSVVQKQDVRTNTAIKNIKKIKLTG	660
Query	750	D 750	
Sbjct	661	D 661	

>emb|CAA67011.1| penicillin-binding protein [Streptococcus pneumoniae]
Length=666

Score = 1141 bits (2952), Expect = 0.0, Method: Composition-based stats. Identities = 583/666 (87%), Positives = 627/666 (94%), Gaps = 0/666 (0%)			
Query	85	VPIAEDATSYNVYAVIDENYKSATGKILYVEKTQFNKVAEVFKYLDMEESYVREQLSQP	144
Sbjct	1	VPIAEDATSYNVYAVID+ YKSATGKILYVE +QFNKVAEVFKYLDM+E+YV+EQL+QP	
Sbjct	1	VPIAEDATSYNVYAVIDKKYKSATGKILYVEDSQFNKVAEVFKYLDMDEAYVKEQLAQP	60
Query	145	NLKQVSFGAKGNIGINYANMMSIKKELEAAEVKGIDFTTSPNRSYPNGQFASSFIGLAQLH	204
Sbjct	61	NL QVSFGAKGNIGINYANMM+IKK+L+ A V+GIDFTT PNRSPNGQFASSFIGLAQLH	
Sbjct	61	NLTQVSFGAKGNIGINYANMMAIKDLKDASVEGIDFTTGPNRSPNGQFASSFIGLAQLH	120

Query	205	ENEDGSKSLLGTSGMESSLNSILAGTDGIITYEKDR LGNIVPGTEQVSQRTMDGKD VYTT ENEDGSKSLLGT G+ESSLN+ILAGTDGIITYEKDR+GNIVPGTE VSQ+T+DGKD VYTT	264
Sbjct	121	ENEDGSKSLLGTGLESSLNTILAGTDGIITYEKDR VGNIVPGTELVSQQTV DGKD VYTT	180
Query	265	ISSPLQSF METQMDAFQEKVKGKYM TATL VSAKTGEILATTQRPTFDADTKEGITEDFVW +SSP+QS FMETQMDAF EKVKGKYM TATL VSAKTGEILATTQRPTF+ADTK+GIT+DFVW	324
Sbjct	181	LSSPVQSF METQMDAFLEKVKGKYM TATL VSAKTGEILATTQRPTFNADTKDG ITKDFVW	240
Query	325	RDILYQSN YEPGSTMKVMM LAAAI DNNTFPGGEVFNSSELKIADATIRDWDVNEGLTGGR RDILYQ NYEPGS MKVM LA+ +IDNNTFPGGE FNSSE KIAD TIRDWDVNEGLTGGR RDILYQGNYEPGSAMKVMTLASSIDDNNTFPGGEYFNSSES KIADVTIRDWDVNEGLTGGR	384
Sbjct	241	RDILYQGNYEPGSAMKVMTLASSIDDNNTFPGGEYFNSSES KIADVTIRDWDVNEGLTGGR	300
Query	385	MMTFSQGFAHSSNVGM TLLEQKMG DATWL DYLNR FKFGV PTRF GLTDEYAG QLPAD NIVN MMTFSQGFAHSSNVG LLE+KMGD TWLDYLNR FKFGV PTRF GLTDEYAG QLPAD NIVN+ MMTFSQGFAHSSNVGT ILL EKMGDT WL DYLNR FKFGV PTRF GLTDEYAG QLPAD NIVS	444
Sbjct	301	MMTFSQGFAHSSNVGT ILL EKMGDT WL DYLNR FKFGV PTRF GLTDEYAG QLPAD NIVS	360
Query	445	IAQSSFGQGI SVTQTQMI R AFTA I ANDGV MLEPKF ISAIYDPNDQ TARKS QKEIVGNPVS IAQSSFGQGI SVTQTQMI R AFTA I ANDGV MLEPKF I+A+YDPNDQ T RKS QKEIVGNPVS IAQSSFGQGI SVTQTQMI R AFTA I ANDGV MLEPKF I TALYDPNDQ T VRKS QKEIVGNPVS	504
Sbjct	361	IAQSSFGQGI SVTQTQMI R AFTA I ANDGV MLEPKF I TALYDPNDQ T VRKS QKEIVGNPVS	420
Query	505	KDAASLT RTNMVLV GTDPV YGT MYNH STG KPTV T VPG QNVAL KSG TA QIA DEKNGGYLVG KDAAS TRT MVLV GTDPV YGT MYNH STG KPTV T VPG QNVAL KSG TA QIA DEKNGGYLVG	564
Sbjct	421	KDAASQTRTQMVLV GTDPV YGT MYNH STG KPIV T VPG QNVAL KSG TA QIA DEKNGGYLVG	480
Query	565	LTDYI FSAV S M SPAEN PDF ILYV TVVQ QPEH YSGIQL GE FANPI LERAS AMK D S L N L QTTA T+YIFS V+M+PAEN PDF ILYV TVVQ QPEH+SGIQL GE FANPI LERAS AMK+SLNLQ+ A PTNYI FSVVAMNP AEN PDF ILYV TVVQ QPEH FSGIQL GE FANPI LERAS AMK E S L N L QSPA	624
Sbjct	481	PTNYI FSVVAMNP AEN PDF ILYV TVVQ QPEH FSGIQL GE FANPI LERAS AMK E S L N L QSPA	540
Query	625	KALEQV SQQSPY PMPSV KDI SPG DLA EELRRN L VQPIV VGT GT KIK N SSAEEG KNL APNQ K L+QV+ +S Y MPS+KDISPG+LAE LRRN+VQPIV VGT GT KIK +S EEG KNL APNQ KNLDQV TTESSYAMPSIK DISPGELAETLRRNIVQPIV VGT GT KIK ETS VEEG KNL APNQ	684
Sbjct	541	KNLDQV TTESSYAMPSIK DISPGELAETLRRNIVQPIV VGT GT KIK ETS VEEG KNL APNQ	600
Query	685	QVLILSDKAEEVPDMY GWK T KETA ET LAK WLNIELE FQGSGSTVQ KQD VR RANTAI KDI KKI QVL+LSDK EE+PDMY GW KETA ET AKWL+IELE F+GSGS VQ KQD VR NTAIK+IKKI QV LLLSDKV E EIPDMY GWK KETA ET FAK WLDIELE FEGSGSIVQ KQD VR NT A I KNI KKI	744
Sbjct	601	QV LLLSDKV E EIPDMY GWK KETA ET FAK WLDIELE FEGSGSIVQ KQD VR NT A I KNI KKI	660
Query	745	TTL LGD 750 LTL LGD	
Sbjct	661	KLT LGD 666	

>gb|AY56840.1| penicillin-binding protein 2X [Streptococcus pneumoniae]
Length=667

Score = 1140 bits (2949), Expect = 0.0, Method: Composition-based stats.
Identities = 585/667 (87%), Positives = 626/667 (93%), Gaps = 0/667 (0%)

Query	84	GVPIAEDATSYN VYAVI DEN YKSATG KI LYVE KTQ FNKVAEV FHK YLD M E S Y VRE QLSQ GVPIAEDATSYN VYAVI D+ YKSATG KI LYVE QFNKVAEV FHK YLD M+E+YV+E QLSQ	143
Sbjct	1	GVPIAEDATSYN VYAVI D+ YKSATG KI LYVE QFNKVAEV FHK YLD M E A YV K E QLSQ	60
Query	144	PNL QVS FGA KGN GITYAN MMS I KKE LEAA EVKG IDFT TSPN RSY P NGQ FASS FIGLA QL PNL QVS FGA KGN GITYAN MMS+I KKE LEAA EVKG IDFT TSPN RSY P NGQ FASS FIGLA QL	203
Sbjct	61	PNL QVS FGA KGN GITYAN MM M A I KKE LET A E VKG IDFT TSPN RSY P NGQ FASS FIGLA QL	120
Query	204	HENEDGSKSLLGTSGMESSLNSILAGTDGIITYEKDR LGNIVPGTEQVSQRTMDGKD VYTT HENEDGSKSLLGTSGMESSLNSILAG TDGI ITYEKDR LGNIVPGTEQVSQ+T+DGKD VYTT HENEDGSKSLLGTSGMESSLNSILAG KDG I ITYEKDR LGNIVPGTEQVSQQTVDGKD VYTT	263
Sbjct	121	HENEDGSKSLLGTSGMESSLNSILAG KDG I ITYEKDR LGNIVPGTEQVSQQTVDGKD VYTT	180
Query	264	TISSPLQSF METQMDAFQEKVKG KYM TATL VSAKTGEILATTQRPTFDADTKEGITEDFV T+SSPLQSF METQMDAF EKVKG KYM TATL VSAKTGEILATTQRPTF+ADTKEGITEDFV	323
Sbjct	181	TISSPLQSF METQMDAFLEKVKG KYM TATL VSAKTGEILATTQRPTFNADTKEGITEDFV	240
Query	324	WRDILYQSN YEPGSTMKVMM LAAAI DNNTFPGGEVFNSSELKIADATIRDWDVNEGLTGGR WRDILYQSN YEPGS MKVM LA+ +IDNNTFP GE FNSSE KIADAT RDWDVN+GLT G	383
Sbjct	241	WRDILYQSN YEPGSAMKVMTLASSIDDNNTFPSGEYFNSSE F KIADAT TRDWDVN DGLTTG	300
Query	384	RMMTFSQGFAHSSNVGM TLLEQKMG DATWL DYLNR FKFGV PTRF GLTDEYAG QLPAD NIV MMTF QGFAHSSNVGM+LLEQKMG DATWL DYL RFKFGV PTRF GLTDEYAG QLPAD NIV	443
Sbjct	301	GMMTFLQGFAHSSNVGMSLLEQKMG DATWL DYL KRFKFGV PTRF GLTDEYAG QLPAD NIV	360
Query	444	NIAQSSFGQGI SVTQTQMI R AFTA I ANDGV MLEPKF ISAIYDPNDQ TARKS QKEIVGNP +IAQSSFGQGI SVTQTQMI R AFTA I ANDGV MLEPKF ISAIYD N+Q+ RKS QKEIVGNP SIAQSSFGQGI SVTQTQML R AFTA I ANDGV MLEPKF ISAIYD TN QSVR KS QKEIVGNP	503
Sbjct	361	SIAQSSFGQGI SVTQTQML R AFTA I ANDGV MLEPKF ISAIYD TN QSVR KS QKEIVGNP	420
Query	504	SKDAASLT RTNMVLV GTDPV YGT MYNH STG KPTV T VPG QNVAL KSG TA QIA DEKNGGYLV SK+FAAS TR +M+L VGT DP+Y GT MYNH TGKP +T VPG QNVA+KSG TA QIA DEKNGGYLV	563
Sbjct	421	SKDAASLT RTNMVLV GTDPV YGT MYNH TGKP +T VPG QNVA+KSG TA QIA DEKNGGYLV	480
Query	564	GLTDYI FSAV S M SPAEN PDF ILYV TVVQ QPEH YSGIQL GE FANPI LERAS AMK D S L N L QTT G T+YIFS V+M+PAEN PDF ILYV TVVQ QPEH YSGIQL GE FANPI LERAS AMK+SLNLQ+ GSTNYI FSVV T MNP AEN PDF ILYV TVVQ QPEH YSGIQL GE FANPI LERAS AMK E S L N L QSPA	623
Sbjct	481	GSTNYI FSVV T MNP AEN PDF ILYV TVVQ QPEH YSGIQL GE FANPI LERAS AMK E S L N L QSPA	540
Query	624	AKALEQV SQQSPY PMPSV KDI SPG DLA EELRRN L VQPIV VGT GT KIK N SSAEEG KNL APN AK L++V+ +S Y MPS+KDISPG+LAE LRRN+VQPIV VGT GT KIK +S EEG NLAPN	683
Sbjct	541	AKNLDKV TTESSYAMPSIK DISPGELAETLRRNIVQPIV VGT GT KIK ETS VEEG TN L APN	600

Query	684	QQVLILSDKAEEVPDMYGWTKETAETLAKWLNLIELEFOGSGSTVOKODVRANTAIKDIKK	743
Sbjct	601	QQVLLLSDKVEEIPDMYGWKKETAETFAKWLDIELEFEGSGSVVQKQDVRTNTAIKNIKK	660
Query	744	ITLTLGD 750	
		I LTLGD	
Sbjct	661	IKLTLGD 667	
>gb AAN32856.1 penicillin-binding protein 2X [Streptococcus pneumoniae]			
Length=661			
Score = 1139 bits (2945), Expect = 0.0, Method: Composition-based stats.			
Identities = 586/661 (88%), Positives = 624/661 (94%), Gaps = 0/661 (0%)			
Query	90	DATSYNVAVIDENYKSATGKILYVEKTQFNKVAEVFKYLDMEESYVREQLSQPNLKQV	149
Sbjct	1	DATSYNVAVIDENYKSATGKILYVEKTQFNKVAEVFKYLDMEESYVREQLSQPNLKQV	60
Query	150	SFGAKGNIGITYANMMSIKKELEAAEVKGIDFTTSPNRSYPNGQFASSFIGLAQLHENEDG	209
Sbjct	61	SFG+KGNIGITYANMMSIKKELE AEVKGIDFTTSPNRSYPNGQFASSFIGLAQLHENEDG	120
Query	210	SKSLLGTSGMESSLNSILAGTDGIITYEKDRGLNIVPGTEQVSQRTMDGKDVTYTTISSPL	269
Sbjct	121	SKSLLGTSGMESSLNSILAGTDGIITYEKDRVGNIVPGTELVSQQTVDGKDVTYTTISSPL	180
Query	270	QSFMETQMDAFQEVKVGKYMATTLSAKTGEILATTQRPTFDADTKEGITEDFVWRDILY	329
Sbjct	181	QSFMETQMDAF EKVKGKYMATTLSAKTGEILATTQRPTF+ADTKEGITEDFVWRDILY	240
Query	330	QSNYEPGSTMVKVMMIAAIIDNNTFPGEVFNSSELKIADATIRDWDVNNEGLTGGRMMTFS	389
Sbjct	241	QSNYEPGS MKVM LA++IDNNTFP GE FNSSE KIADAT RDWDVN+GLT G MMTF	300
Query	390	QGFAHSSNVGM+LLEQKMGDATWLDYL RFKFGVPTRFGLTDEYAGQLPADNIVNIAQSS	449
Sbjct	301	QGFAHSSNVGM+LLEQKMGDATWLDYL RFKFGVPTRFGLTDEYAGQLPADNIV+IAQSS	360
Query	450	FGQGISVTQTOIMIRFTAIAANDGVMLEPKFISAIYDPNDQTARKSQKEIVGNPVSKAAS	509
Sbjct	361	FGQGISVTQTOQM+RAFTAIANDGVMLEPKFISAIYD N+Q+ RKSQKEIVGNPVSKAAS	420
Query	510	LTRTNMVLVGTDPVYGTMYNHSTGKPTVTVPQONVALSGTAQIADEKNGGYLVGLTDYI	569
Sbjct	421	TR +M+LVGTD+YGTMYNH TGKP +TVPGQNV+A KSGTAQIADEKNGGYLVG T+YI	480
Query	570	FSAVSMSPAENPDFILYVTVQQPEHYSGIQLGEFANPILERASAMKDSLNLQTTAKALEQ	629
Sbjct	481	FS V+M+PAENPDFILYVTVQQPEHYSGIQLGEFA PILERASAMK+SLNLQ+ AK L++	540
Query	630	FSVVTMNPSPAENPDFILYVTVQQPEHYSGIQLGEFATPILERASAMKESLNQSPAKNLDK	
Sbjct	541	VSQQSPYPMPSVKDISPGDLAEELRRNLVQPIVVGTGKIKNSSAEEGKNLAPNQQVLIL	689
Sbjct	541	V+ +S Y MPS+KDISPG+LAE LRRN+VQPIVVGTGKIK +S EEG NLAPNQQVL+L	600
Query	690	VTTESSYAMPSIKDISPGELAEALRRNIVQPIVVGTGKIKETSVEEGTNLAPNQQVLL	
Sbjct	601	SDKAEEVPDMYGWTKETAETLAKWLNLIELEFOGSGSTVOKQDVRANTAIKDIKKITLTLG	749
Sbjct	601	SDK EE+PDMYGW KETAET AKWL+IELEF+GSGS VQKQDVR NTAIK+IKKI LTG	
Sbjct	601	SDKVEEIPDMYGWKKETAETFAKWLDIELEFEGSGSVVQKQDVRTNTAIKNIKKIKLTG	660
Query	750	D 750	
Sbjct	661	D 661	

>gb|ABB46508.1| penicillin binding protein 2x [Streptococcus pneumoniae]

Query	94	YNVYAVIDENYKSATGKILYVEKTQFNKVAEVFKYLDMEESYVREQLSQPNLKQVSFGA	153
Sbjct	1	YNVYAVIDENYKSATGKILYVEKTQFNKVAEVFKYLDMEESYVREQLSQPNLKQVSFGA	60
Query	154	KGNIGITYANMMSIKKELEAAEVKGIDFTTSPNRSYPNGQFASSFIGLAQLHENEDGSKSL	213
Sbjct	61	KGNIGITYANMMSIKKELEAAEVKGIDFTTSPNRSYPNGQFASSFIGLAQLHENEDGSKSL	120
Query	214	LGTSGMESSLNSILAGTDGIITYEKDRGLNIVPGTEQVSQRTMDGKDVTYTTISSPLQSF	273
Sbjct	121	LGTSGMESSLNSILAGTDGIITYEKDR+GNIVPGTE VSQ+T+DGKDVTYTT+SSPLQSF	180
Query	274	ETQMDAFQEVKVGKYMATTLSAKTGEILATTQRPTFDADTKEGITEDFVWRDILYQSN	333
Sbjct	181	ETQMDAFLEKVGKYMATTLSAKTGEILATTQRPTFNADTKEGITEDFVWRDILYQSN	240

Query	334	EPGSTMVKMMLAAAIDNNTFPGGEVFNSSELKIAADATIRDWDVNNEGLTGGRMMTFSQGFA	393
Sbjct	241	EPGS MKVM LA++IDNNTFP GE FNSSE KIADAT RDWDVN+GLT G MMTF QGFA	300
Query	394	HSSNVGMTLLEQKMGM DATWLDYLNRFKFGVPTRFGLTDEYAGQLPADNIVNIAQSSFGQG	453
Sbjct	301	HSSNVGM+LLEQKMGM DATWLDYL RFKFGVPTRFGLTDEYAGQLPADNIV+IAQSSFGQG	360
Query	454	ISVTQTQMIRAFTAIANDGVMLEPKFISAIYDPNDQTARKSQKEIVGNPVSKDAASLTTRT	513
Sbjct	361	ISVTQTQM+RAFTAIANDGVMLEPKFISAIYD N+Q+ RKSQKEIVGNPVSK+AAS TR	420
Query	514	NMVLVGTDPVYGTMYNHS TGKPTVTPGQNVALKSGTAQIADEKNGGYLVGLTDYIFSAV	573
Sbjct	421	+M+L VGTDP+YGTMYNH TGKP +TV PGQNVA+KSGTAQIADEKNGGYLV T+YIFS V	480
Query	574	HMILVGTDP LYGTMYNHYTGKPIITVPGQNVAVKSGTAQIADEKNGGYLVGSTNYIFSVV	600
Sbjct	481	SMSPAENPDFI LYVTVQQPEHYSIGIQLGEFANPILERASAMKDSLNLQTTAKALEQVSQQ	633
		+M+PAENPDFI LYVTVQQPEHYSIGIQLGEFA PILERASAMK+SLNLQ+ AK L++V+ TMNPAENPDFI LYVTVQQPEHYSIGIQLGEFATPILERASAMKESLNLQSPAKNLKDVTTE	540
Query	634	SSYAMPSIKDISPGELAEALRRNIVQPIVVGTKIKETSVEEGTNLAPNQQVLLSDKV	693
Sbjct	541	SPYPMPSVKDISPGDLAEE LRRNLVQPIVVGTKIKKNSSAEEGKNLAPNQQVLLSDKA	600
Query	694	S Y MPS+KDISPG+LAE LRRN+VQPIVVGTKIK +S EEG NLAPNQQVLLSDKV	750
Sbjct	601	EEIPDMYGW KETAET AKWL+IELEF+GSGS VQKQDVR NTAIK+I KI LTLGD	657

>gb|AY56855.1| penicillin-binding protein 2X [Streptococcus pneumoniae]
Length=669

Score = 1135 bits (2935), Expect = 0.0, Method: Composition-based stats.
Identities = 580/669 (86%), Positives = 626/669 (93%), Gaps = 0/669 (0%)

Query	82	RNGVPIAEDATS NVYAVIDENYKSATGKILYVEKTQFNKVAEVFHKYLDMEESYVREQL	141
Sbjct	1	RNGVPIAEDATS NVYAVID+ YKSATGKILYVE QFNKVAEVFHKYLDM+E+YV+EQL	60
Query	142	SQP NLKQVSFGAKGNGITYANMMSIKKELEAAEVKGIDFTTSPNRSYPNGQFASSFIGLA	201
Sbjct	61	SQP NL QVSFGAKGNGITYANMM+IKK+L+ A V+GIDFTTSPNRSYPNGQFASSFIGLA	120
Query	202	SQP NLTQVSFGAKGNGITYANMMAIKKDLKDASVEGIDFTTSPNRSYPNGQFASSFIGLA	120
Sbjct	121	QLHENEDGSKSLLGTSGMESSLNSILAGTDGI ITYEKDR LGNIVPGTEQVSQRTMDGKDV	261
		QLHENEDGSKSLLGTSG+ESSLN+ILAGTDGI ITYEKDR LGNIVPGTEQVSQ+T+DGKDV	180
Query	262	QLHENEDGSKSLLGTSGLESSLNTILAGTDGI ITYEKDR LGNIVPGTEQVSQQTVDGKDV	321
Sbjct	181	YTTISSLPLQSFMETQMDAFQEKVKGKYMTATLVSAKTGEI LATTQRPTFDADTKEGITED	240
		YTT+SSPLQSFMETQMDAF EKVKGKYMTATLVSAKTGEI LATTQRPTF+ADTKEGITED	240
Query	322	YTTLSSPLQSFMETQMDAFLEKVKGKYMTATLVSAKTGEI LATTQRPTFNADTKEGITED	381
Sbjct	241	FVWRDILYQSNYEPGSTMVKMMLAAAIDNNTFPGGEVFNSSELKIAADATIRDWDVNNEGLT	300
		FVWRDILYQSNYEPGS KVMM LA++IDNNTFP GE FNSSE KIADAT RDWDVN GLT	
Query	382	FVWRDILYQSNYEPGS AFKVMM LASSIDNNTFPSGEYFNSSEFKIADATTRDWDVNAGLT	441
Sbjct	301	TGGMMTFLQGFAHSSNVGTSLLQKMGM DATWLDYLKRFKFGVPTRFGLTDEYAGQLPADN	360
Query	442	TGGMMTFLQGFAHSSNVGTSLLQKMGM DATWLDYLKRFKFGVPTRFGLTDEYAGQLPADN	501
Sbjct	361	IVNIAQSSFGQGQGISVTOMIRAFTAIANDGVMLEPKFISAIYD PNDQTARKSQKEIVGN	420
		IV+IAQSSFGQGQGISVTQTQM+RAFTAIANDGVMLEPKFISAIYD N+Q+ RKSQKEIVGN	
Query	502	IVSIAQSSFGQGQGISVTQTQM+RAFTAIANDGVMLEPKFISAIYD N+Q+ RKSQKEIVGN	561
Sbjct	421	IVSIAQSSFGQGQGISVTQTQM+RAFTAIANDGVMLEPKFISAIYD N+Q+ RKSQKEIVGN	480
Query	562	PVS KDAASLRTNMVLVGTDPVYGTMYNHS TGKPTVTPGQNVALKSGTAQIADEKNGGY	621
Sbjct	481	PVS KDAASLRTNMVLVGTDPVYGTMYNHS TGKPTVTPGQNVALKSGTAQIADEKNGGY	540
Query	622	PVS KEAASLRTNMVLVGTDPVYGTMYNHS TGKPTVTPGQNVALKSGTAQIADEKNGGY	681
Sbjct	541	PVS KEAASLRTNMVLVGTDPVYGTMYNHS TGKPTVTPGQNVALKSGTAQIADEKNGGY	600
Query	682	LVGLTDYIFSAVSMSPAENPDFI LYVTVQQPEHYSIGIQLGEFANPILERASAMKDSLNLQ	741
Sbjct	601	LVGLTDYIFSAVSMSPAENPDFI LYVTVQQPEHYSIGIQLGEFANPILERASAMKDSLNLQ	660
Query	742	LVGLTDYIFSAVSMSPAENPDFI LYVTVQQPEHYSIGIQLGEFANPILERASAMKDSLNLQ	660
Sbjct	661	KKI LTLDG KKI LTLDG	669

Database: All non-redundant GenBank CDS translations+PDB+SwissProt+PIR+PRF excluding environmental samples from WGS projects
Posted date: May 31, 2007 5:55 PM
Number of letters in database: 146,036
Number of sequences in database: 262
Lambda K H
0.313 0.130 0.362
Gapped
Lambda K H
0.267 0.0410 0.140
Matrix: BLOSUM62
Gap Penalties: Existence: 11, Extension: 1
Number of Sequences: 262
Number of Hits to DB: 1868
Number of extensions: 66
Number of successful extensions: 3
Number of sequences better than 10: 1
Number of HSP's better than 10 without gapping: 0
Number of HSP's gapped: 1
Number of HSP's successfully gapped: 1
Length of query: 750
Length of database: 146036
Length adjustment: 77
Effective length of query: 673
Effective length of database: 125862
Effective search space: 84705126
Effective search space used: 84705126
T: 11
A: 40
X1: 16 (7.2 bits)
X2: 38 (14.6 bits)
X3: 64 (24.7 bits)
S1: 42 (20.8 bits)
S2: 48 (23.1 bits)